

Publication No. US20030104482A1
GENERAL INFORMATION:
APPLICANT: Immune Corp.
APPLICANT: Bird, Timothy
APPLICANT: Vice, G.D.
TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
FILE REFERENCE: 2889-US
CURRENT APPLICATION NUMBER: US/10/299,327
PRIORITY FILING DATE: 2002-11-18
PRIORITY FILING DATE: US/09/509,802
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent version 3.0
SEQ ID NO 2
LENGTH: 786
TYPE: PRT
ORGANISM: Mus sp.
US-10-299-327-2

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 3.9e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNPSWVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGEIIVE 170
DB 434 DLVLD-SSASLHLAVEAQGECEVKMLLNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFFHYAVQ-GDNSQVQLQIGRNAVAGLNQVNOGTLPLHLAQ 229
DB 491 LILARKTSVNAKDEQMTALHFAQNGDEASTRLLEKN--ASVNEVDEGRTPMHIVACQ 548
QY 230 LKQENVRVLLCNARCINMGNGY-PIHSAMFSGKCAEMISDSQHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVADVGLQGDAMLPHYAMQGHLPVYKLAQPGVSVNAQ-TLDR 607
QY 289 SPLHMAK--NAEMARMLKRCGNVSTSSAGNTALHGVMMRRPDCATVLLTHGANADA 345
DB 608 TPLHLAAGRGHYRVARILDLCSQVNICSLQAOPTPLHVAETGHTSTALLHHRGAKGA 667
QY 346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTDPNDFGTPPLFLASKIGKIQ----- 397
DB 668 LTSEGYTALHLAONGHLATVLLIEKADVMARGLNQTALHLAARGHSEVEBELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

RESULT 14
US-10-128-174-13
Sequence 13, Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
PRIORITY FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 13
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-13

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 3.9e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNPSWVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGEIIVE 170

DB 434 DLVLD-SSASLHLAVEAQGECEVKMLLNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFFHYAVQ-GDNSQVQLQIGRNAVAGLNQVNOGTLPLHLAQ 229
DB 491 LILARKTSVNAKDEQMTALHFAQNGDEASTRLLEKN--ASVNEVDEGRTPMHIVACQ 548
QY 230 LKQENVRVLLCNARCINMGNGY-PIHSAMFSGKCAEMISDSQHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVADVGLQGDAMLPHYAMQGHLPVYKLAQPGVSVNAQ-TLDR 607
QY 289 SPLHMAK--NAEMARMLKRCGNVSTSSAGNTALHGVMMRRPDCATVLLTHGANADA 345
DB 608 TPLHLAAGRGHYRVARILDLCSQVNICSLQAOPTPLHVAETGHTSTALLHHRGAKGA 667
QY 346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTDPNDFGTPPLFLASKIGKIQ----- 397
DB 668 LTSEGYTALHLAONGHLATVLLIEKADVMARGLNQTALHLAARGHSEVEBELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

RESULT 15
US-10-128-174-31
Sequence 31, Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
PRIORITY FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patent version 3.1
SEQ ID NO 31
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-31

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 3.9e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNPSWVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGEIIVE 170
DB 434 DLVLD-SSASLHLAVEAQGECEVKMLLNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFFHYAVQ-GDNSQVQLQIGRNAVAGLNQVNOGTLPLHLAQ 229
DB 491 LILARKTSVNAKDEQMTALHFAQNGDEASTRLLEKN--ASVNEVDEGRTPMHIVACQ 548
QY 230 LKQENVRVLLCNARCINMGNGY-PIHSAMFSGKCAEMISDSQHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVADVGLQGDAMLPHYAMQGHLPVYKLAQPGVSVNAQ-TLDR 607
QY 289 SPLHMAK--NAEMARMLKRCGNVSTSSAGNTALHGVMMRRPDCATVLLTHGANADA 345
DB 608 TPLHLAAGRGHYRVARILDLCSQVNICSLQAOPTPLHVAETGHTSTALLHHRGAKGA 667
QY 346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTDPNDFGTPPLFLASKIGKIQ----- 397
DB 668 LTSEGYTALHLAONGHLATVLLIEKADVMARGLNQTALHLAARGHSEVEBELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

Search completed: May 26, 2005, 14:51:06

[illegible]

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; PRIOR FILING DATE: 2002-02-21
;
; NUMBER OF SEQ ID NOS: 47374
;
; SEQ ID NO 4998

```

SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 42.3%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 396 LQDLMHSRRKRAFLIGSMRDEKRTDHLCLDGGVKGILITQLIAIEKASGVA TKD 455
DB 1 LQDLMHSRRKRAFLIGSMRDEKRTDHLCLDGGVKGILITQLIAIEKASGVA TKD 60
QY 456 LEPDVAAGTSGGILALAILHKSMAVYRGMYFRMKDEVPFGSRPYESGPLEEFLKRFGE 515
DB 61 LEPDVAAGTSGGILALAILHKSMAVYRGMYFRMKDEVPFGSRPYESGPLEEFLKRFGE 120
QY 516 HTMTDVRKPKWLTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRPAPQSPDQV 575
DB 121 HTMTDVRKPKWLTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRPAPQSPDQV 180
QY 576 WRARSSGAAPTYFRPRGRFLDGGILANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 635
DB 181 WRARSSGAAPTYFRPRGRFLDGGILANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 240
QY 636 VSLGTSRSPQVPVTCVDFPRSPNPMELAKTVFGAKELGKVVVDCCTDPDGRP 687
DB 241 VSLGTSRSPQVPVTCVDFPRSPNPMELAKTVFGAKELGKVVVDCCTDPDGRP 292

RESULT 7
US-10-369-493-6665
; Sequence 6665, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6665
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6665

Query Match 17.9%; Score 647.5; DB 15; Length 1071;
Best Local Similarity 27.0%; Pred. No. 1.3e-49;
Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

QY 69 FRLFOLELEADALVNFHOYSSQLLPYESSPOVLAHTEVL-----QHLTDLIRNHPSSVAH 124
DB 315 FSLFRATDKKDLMDLHLCOBKSFSLFTSLDMSTMRADILNSKIBELVIOURLRPHYMIH 374
QY 125 LAVELEIRBCEFHHSRI-----ISCANCAENBEGCPTLHACKRGDEILVELVOY 174
DB 375 VALATDRLLFFSDGMKIKTMMETLEPESSQRLCCHENCYPAHLALTMROKIVERLEL 434
QY 175 CHQMDVTVYKGTGVHYAVQSGNSQVQLQLGKNAVAG---LQVANNQGLTPLHLACQLG 231
DB 435 DPTLFCEETDAGKGVNHHV---NSSFCAQIIMDRCPASQHFIDERNMDQSPINEAVSTA 491

QY 232 KQEMVAVLLICNARCINMGNGPYPIISAMKFSQKCAEMTISM-----DSS 277
DB 492 KPLVATFL-----IGKAFPTRGDRNELFVAMTSKNAQSGVEVVLTDKP 535
QY 278 QHSKDPYRGASPLHAKNAEMARMLLKR-----GCNVNSTSSAGNTALHYGVWRNRPDCA 333
DB 536 EIANERDALGNSAIHYALVYESINALLNRKVELGLDIDVGNANAGERLILLFITTRKDDL 595
QY 334 IVLLT---HGANDARGEHGTPLHLAMS-----KQNVEMIKALIVFGAEVDPNDPGET 385
DB 596 PLIVTLVYHAGANNANVADPHGNTALHKSAAVLDAKTIISLECVKFLISAGSNPKINLRGES 655
QY 386 PTLASKIGKLDQDLMHSRA---RKPAFLG-----SMRDE----- 418
DB 656 PRHLAASL-QNOMELAILKAAGATRCPKGYKGRSNCRDHSCSAEDEYEETLOKIRIGNE 714
QY 419 -----KRTDHLCLDGGVKGILITQLIAIEKASGVA 452
DB 715 SDYEKTEFTASEKLNIDQTLDSRRGKAKVNLISMDGGGIRGLVITQLIAIEBRIGDD 774
QY 453 TKDLFDVVAAGTSGGILALAILHKSMAVYRGMYFRMKDEVPFG-SRYPESGPLEEFLKR 511
DB 775 IFKYFDMASGTSGLIMGLATGKSIREMQOTYLLKORVFDGIMPEPYDTQLEKTIOD 834
QY 512 EREBHTKMTDVRKPKWLTGTLSDRQPAELHLFRNYDAPETVREPRFNQVNLRPAPQS 571
DB 835 QFQGTGT-VWEIPYRLMISAVNSEKLPVRLMARANYKPAKV-----ABETPK 881
QY 572 DQVWRARSSGAAPTYFRPN-GRFLDGGILANNPTLDAMTEIHEYNODLIRKGOANKVK 630
DB 882 EMLPMALRRSTAPVLFKSESDRYIDGGIISNPALDMSVHAYNRLOLSGRSDAV 941
QY 631 KLSIVSLGTSRSPQVPVTCVDFR--PSNPMELAKTVFGAKELGKVVVDCCTDPDGRP 687
DB 942 QMNVLVSPFGT---QIPSTVTEFLSLDSSNPLQSIITI---KULAMFIDQATASGAP 994

RESULT 8
US-10-369-493-6689
; Sequence 6689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6689
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6689

Query Match 17.5%; Score 634.5; DB 15; Length 1023;
Best Local Similarity 24.2%; Pred. No. 1.8e-48;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

QY 37 RVAREGQILIFONTNRTWDCVAVNPRNSQSGRFLFOLELEAD--ALVNFHOYSSQLLP 94
DB 204 RAKEBREL---KKKPLXHLAITLYNNENKEYVMSLFRSHKLADVVALCERCRENPELFRV 260
QY 95 YESSPOV---LHTEVLQHLTDLIRNHPSSVAHLAVELEIRBCEFH---SRITSCANCAE 148
DB 261 FPNQNVIKQVLYHT---IFHELRDMTWKSVHISKIGILFEYENMKHKJLKKYINLTV 315

Db 102 LCNARCNIMGPNGYPIYSAMKFSQKGCAMTISMSOISHSDPRYGASPLHMAKNAEMA 161
Qy 301 RMLLRKGCNVNSTSSAGNTALHVGWVRNRPDCAIVLLTHGANADARGEHNTPLHIAWSK 360
Db 162 RMLLRKGCNVNSTSSAGNTALHVGWVRNRPDCAIVLLTHGANADARGEHNTPLHIAWSK 221
Qy 361 DNVEIMKALIVGAEVDTNDPGEPTPLASKIGK----- 395
Db 222 DNVEIMKALIVGAEVDTNDPGEPTPLASKIGKGLVTRKAILTLRTVGAECYCPPIHG 281
Qy 396 -----LQDLMIHSRAKPAFLGSMRDEKRTDHL 425
Db 282 VPBAQGSAAHPHFSLERAQPPISLNNLELODLMIHSRAKPAFLGSMRDEKRTDHL 341
Qy 426 LCLDGGVAGLITLITLILAEKASGATKDLPMWAGTSGTGLALATLHSHSMATWRCM 485
Db 342 LCLDGGVAGLITLITLILAEKASGATKDLPMWAGTSGTGLALATLHSHSMATWRCM 401
Qy 486 YFRMKDEVRGSRPYESGPLEEFLKREGEHTMTDVRKPKWMLTGLSDROPALHLFR 545
Db 402 YFRMKDEVRGSRPYESGPLEEFLKREGEHTMTDVRKPKWMLTGLSDROPALHLFR 461
Qy 546 NYDAPETVREPRNQNVLPRPAQPSDQVWRAARSSGAAPTYFRNGRFLDGLLANNP 605
Db 462 NYDAPETVREPRNQNVLPRPAQPSDQVWRAARSSGAAPTYFRNGRFLDGLLANNP 521
Qy 606 TLDAMTEIHEYNODLIRKQANKVKLSTVSLGTGRSPQVPTCVDFRPSNPWELAT 665
Db 522 TLDAMTEIHEYNODLIRKQANKVKLSTVSLGTGRSPQVPTCVDFRPSNPWELAT 581
Qy 666 VFGAKELGKVVVDCCTDPDGR 686
Db 582 VFGAKELGKVVVDCCTDPDGR 602

RESULT 5

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/09/927,180

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 394 amino acids

TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 57.6%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 4,1e-182;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOFPGRLVNTFSGVNTLPSNPFRVKEVAVADTSSDRVREBQQLIFONTPTMTDCVLY 60
Db 1 MOFPGRLVNTFSGVNTLPSNPFRVKEVAVADTSSDRVREBQQLIFONTPTMTDCVLY 60
Qy 61 NPNRSOSGFRPLQLEHADALVNFHOYSQQLPFYESSQVLAETVLOLTLIRNHPSM 120
Db 61 NPNRSOSGFRPLQLEHADALVNFHOYSQQLPFYESSQVLAETVLOLTLIRNHPSM 120
Qy 121 SVAHLAVELGIRECFHRSIIISCANCAENEBECTPLHLACRKGDEIIVELYCHTQMD 180
Db 121 SVAHLAVELGIRECFHRSIIISCANCAENEBECTPLHLACRKGDEIIVELYCHTQMD 180
Qy 181 VTDYKGETVFNHYAVOGDNSQVLOLGRNAVAGLQVNNQGLTPHLACQLGKQEMRVLL 240
Db 181 VTDYKGETVFNHYAVOGDNSQVLOLGRNAVAGLQVNNQGLTPHLACQLGKQEMRVLL 240
Qy 241 LCNARCNIMGPNGYPIHSAMKFSQKGCAMTISMSOISHSDPRYGASPLHMAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAMKFSQKGCAMTISMSOISHSDPRYGASPLHMAKNAEMA 300
Qy 301 RMLLRKGCNVNSTSSAGNTALHVGWVRNRPDCAIVLLTHGANADARGEHNTPLHIAWSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGWVRNRPDCAIVLLTHGANADARGEHNTPLHIAWSK 360
Qy 361 DNVEIMKALIVGAEVDTNDPGEPTPLASKIG 394
Db 361 DNVEIMKALIVGAEVDTNDPGEPTPLASKIG 394

RESULT 6

US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA: US/09/927,180

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 19:

```

QY      600  LLANNPLTDANTEIHEYNODILIRGQANKVKKLSTIVSLGTRSPQVPTCVDPFRPSNP 653
Db      601  |||||||
        601  LLANNPLTDANTEIHEYNODILIRGQANKVKKLSTIVSLGTRSPQVPTCVDPFRPSNP 660
QY      660  WLAKTVEGAKELGKRVVDCCTDPDGRP 687
Db      661  |||||||
        661  WLAKTVEGAKELGKRVVDCCTDPDGRP 688

RESULT 3
US-09-927-180-2
; Sequence 2, Application US/099272180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
;          Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 752 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match      91.2%; Score 3302.5; DB 9; Length 752;
Best Local Similarity 90.4%; Pred.No.1.7e-293;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY      1  MOFGRLVNTSGVNNLPNSNPRVVEVAVADTSDRREBSQLLFONTPRTMDCVLA 60
Db      1  MGFGRVLNLTSSVNNLPNSNPRVVEISVADTSHRVRREBSQLLFQNASRRTMDCVLA 60
QY      61  NPNRSQSGFRLFQLELEADALVNFQVYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
Db      61  SPRNHSQFRLFQLESEADALVNFQPFSSQLPFFYESSQVLHVEVLQHLSLIRSHPSW 120
QY      121  SVAHLAVELGIRECHHSRIISCANCAENBEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db      121  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 180
        121  TVTHLAVELGIRECHHSRIISCANSTENEBGCTPLHLACRKGDEIILVELVQYCHAQMD 180
QY      181  VTDYKGEIVFHAQGDNSQVQLLGRNAVGLNVNNGQLTFLHLAQLQKGEQVRYLL 240
Db      181  VTDNKGEIATFAHAQGDNSQVQLLQKNASAGLNVNNGQLTFLHLAQLQKGEQVRYLL 240
        181  VTDNKGEIATFAHAQGDNSQVQLLQKNASAGLNVNNGQLTFLHLAQLQKGEQVRYLL 240

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[illegible]

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RESULT 4
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108, 260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match      75.2%; Score 2723; DB 15; Length 667;
Best Local Similarity 73.3%; Pred. No. 2,1e-240;
Matches 543; Conservative 2; Mismatches 2; Indels 194; Gaps 2,

QY      1 MQFGRLLVNTSGVTNLFSPNPRVKEAVADYTSDDRVRREGCOLIFONTENRTDCTVLV 60
DB      1 MQFGRLLVNTSGVTNLFSPNPRVKEAVADYTSDDRVRREGCOLIFONTENRTDCTVLV 60
QY      61 NPNRSQSGFRLLFOLELEADALVNFHOVSQLLPFYESSQVLAHREVLQHLTDLRNHPSW 120
DB      61 YPRNSQSGFRLLFOLELEADALVNFHOVSS----- 89
QY      121 SVAHLAVELGIRECFHSHRIISCANCANENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB      90 ----- 89
QY      181 VTDYKGETVFHYAVQGDNSQVTLQLRNAVAVAGLNQVNNQGLTPLHLACQLGKQENVRVLL 240
DB      90 -----QLGKQENVRVLL 101
QY      241 LCNARCNIMGNGVPIHSAMKFSQKGCAMETIISMDSSQIHSKDPYRGASPLHAKNAEMA 300

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LENGTH: 687 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 US-09-927-180-21

Query Match 100.0%; Score 3620; DB 9; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFGRVLTFSFGVNTLFSNPFVKEVAVADYSSDRVEBQQLIFONTNRTMDCVLV 60
 DB 1 MGFGRVLTFSFGVNTLFSNPFVKEVAVADYSSDRVEBQQLIFONTNRTMDCVLV 60
 QY 61 NPNRSQSGRFLQBLEADALVNFHQSSQLLPFYESSQVLTETVLQHLTDLIRNHP 120
 DB 61 NPNRSQSGRFLQBLEADALVNFHQSSQLLPFYESSQVLTETVLQHLTDLIRNHP 120
 QY 121 SYAHLAVELGIRECFHSRIISCANCAENEBGCTPLHLACRGDGEILVELVOYCHTQMD 180
 DB 121 SYAHLAVELGIRECFHSRIISCANCAENEBGCTPLHLACRGDGEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQDNSQVLLIGRNAVAGLNQVNNQGLTPHLACQLGQEWVRVLL 240
 DB 181 VTDYKGETVFHYAVQDNSQVLLIGRNAVAGLNQVNNQGLTPHLACQLGQEWVRVLL 240
 QY 241 LCNARCNIMGPNGPYIHSAMKFSQKGCAMTISMSQSQHSKDPKRYGASPLHMAKNAEMA 300
 DB 241 LCNARCNIMGPNGPYIHSAMKFSQKGCAMTISMSQSQHSKDPKRYGASPLHMAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHVGWRNRPDCAIVLLTHGANADARGEHTPLHLAMSK 360
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 QY 361 DNVEIMIKALIVGAEDVTENDFGETPTFLASKIGKLQDLMIHSRAKPAFIIGSRWDER 420
 DB 361 DNVEIMIKALIVGAEDVTENDFGETPTFLASKIGKLQDLMIHSRAKPAFIIGSRWDER 420
 QY 421 THDHLICLDGGGVKGLITLQLLIAIKASGVAATKDLFDWAGTSTGGIALLAIIHSK 480
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 DB 541 LHLFRNYDAPETVREBRFNQVNLRRPAPSDQLVWRAARSSGAATYFRPNGRFLDGL 600
 QY 601 LANNPLDAMTEIHEYNQDLIRKGOAKYKLSIVVSLGTGRSPQVPTCVDFRPSNFW 660
 DB 601 LANNPLDAMTEIHEYNQDLIRKGOAKYKLSIVVSLGTGRSPQVPTCVDFRPSNFW 660
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 DB 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 2
 US-09-927-180-23

Sequence 23, Application US/09927180
 Patent No. US20020106364A1

GENERAL INFORMATION:
 APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge

STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/927,180
 FILING DATE: 09-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/519,223
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 688 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
 US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 9; Length 688;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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 DB 361 DNVEIMIKALIVGAEDVTENDFGETPTFLASKIGK-LQDLMIHSRAKPAFIIGSRWDER 420
 QY 420 RTHDHLICLDGGGVKGLITLQLLIAIKASGVAATKDLFDWAGTSTGGIALLAIIHSK 479
 DB 420 RTHDHLICLDGGGVKGLITLQLLIAIKASGVAATKDLFDWAGTSTGGIALLAIIHSK 480
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 DB 480 AYRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTLGTLSDRQPAE 540
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 DB 540 ELHLFRNYDAPETVREBRFNQVNLRRPAPSDQLVWRAARSSGAATYFRPNGRFLDGL 600

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 93.6667 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
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Scoring table: BLOSUM62
Gapop 10.0 , Gapec 0.5

Searched: 146209 segs, 344972447 residues
Total number of hits satisfying chosen parameters: 146209

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3620	100.0	687	9 US-09-927-180-21	Sequence 21, Appl
2	3606.5	99.6	688	9 US-09-927-180-23	Sequence 23, Appl
3	3302.5	91.2	752	9 US-09-927-180-2	Sequence 2, Appl1
4	2723	75.2	667	15 US-10-108-260A-3778	Sequence 3778, Ap
5	2084	57.6	394	9 US-09-927-180-17	Sequence 17, Appl
6	1531	42.3	292	9 US-09-927-180-19	Sequence 19, Appl
7	647.5	17.9	1071	15 US-10-369-493-6865	Sequence 6865, Ap
8	634.5	17.5	1023	15 US-10-369-493-6689	Sequence 6689, Ap
9	634.5	17.5	1023	15 US-10-369-493-6690	Sequence 6690, Ap
10	324.5	9.0	468	15 US-10-369-493-4998	Sequence 4998, Ap
11	324	9.0	1330	15 US-10-108-260A-3237	Sequence 3237, Ap
12	302	8.3	786	14 US-10-164-080-2	Sequence 2, Appl1
13	302	8.3	786	14 US-10-299-327-2	Sequence 2, Appl1

14	302	8.3	786	14	US-10-128-174-13	Sequence 13, Appl
15	302	8.3	786	14	US-10-128-174-31	Sequence 31, Appl
16	302	8.3	786	14	US-10-128-174-32	Sequence 32, Appl
17	302	8.3	786	14	US-10-128-174-33	Sequence 33, Appl
18	302	8.3	787	10	US-09-866-050A-334	Sequence 334, App
19	301.5	8.3	347	14	US-10-128-174-30	Sequence 30, Appl
20	300.5	8.3	1724	9	US-09-964-899-43	Sequence 43, Appl
21	300	8.3	1762	14	US-10-205-194-117	Sequence 117, App
22	296	8.2	1094	17	US-10-479-764-22	Sequence 22, Appl
23	296	8.2	3913	15	US-10-334-143-45	Sequence 45, Appl
24	290	8.0	720	15	US-10-433-794-20	Sequence 20, Appl
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26	290	8.0	765	14	US-10-128-174-34	Sequence 34, Appl
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28	290	8.0	765	14	US-10-128-174-36	Sequence 36, Appl
29	290	8.0	765	14	US-10-128-174-37	Sequence 37, Appl
30	290	8.0	765	14	US-10-128-174-38	Sequence 38, Appl
31	290	8.0	765	14	US-10-128-174-39	Sequence 39, Appl
32	290	8.0	765	14	US-10-128-174-40	Sequence 40, Appl
33	290	8.0	765	14	US-10-128-174-41	Sequence 41, Appl
34	290	8.0	765	14	US-10-128-174-42	Sequence 42, Appl
35	290	8.0	765	14	US-10-128-174-43	Sequence 43, Appl
36	290	8.0	765	14	US-10-128-174-44	Sequence 44, Appl
37	290	8.0	765	15	US-10-182-243-56	Sequence 56, Appl
38	284.5	7.9	784	14	US-10-164-080-7	Sequence 7, Appl1
39	284.5	7.9	784	15	US-10-258-951-70	Sequence 70, Appl
40	282.5	7.8	784	14	US-10-354-353-38	Sequence 38, Appl
41	282.5	7.8	784	14	US-10-128-174-12	Sequence 12, Appl
42	282.5	7.8	784	14	US-10-658-904-2	Sequence 2, Appl1
43	279.5	7.7	784	16	US-10-648-593-153	Sequence 153, App
44	278.5	7.7	1053	15	US-10-291-172-343	Sequence 343, App
45	278.5	7.7	1053	15	US-10-221-278-343	Sequence 343, App

ALIGNMENTS

RESULT 1
US-09-927-180-21
Sequence 21, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

QY 241 LCNARCNMGNGYPIHSAMKESQKGCABMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAMKESQKGCABMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDFGETPFLASKIG 394
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DB 421 RTHDLHLLCUDGGVGLVLIQIIILATEKASGVATKDLFDWVAGTSTGGILALAILHLSKM 480
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
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QY 601 LIANPTLDAMTEIHEYNODLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
DB 601 LIANPTLDAMTEIHEYNODLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 15

US-08-555-568B-17
; Sequence 17, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match 57.5%; Score 2084; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 1.9e-216;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-2

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Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-2

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Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

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DB 1 MOFFGRLVNTLSSVNTLFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
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DB 361 DNWEMIKALIVFGAEVDTNDFGETPFAFWASKISKQLQDLMIHSRARKPAFILGSMRDEK 420
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DB 421 RIHDHLLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHKSXM 480
QY 481 AYMRGMVFMKDEVPFRGSPYESSGPLEEFKREFGEHTKMTDVRPKVMTLGTSLDRQPA 540
DB 481 AYMRGVYFMKDEVPFRGSPYESSGPLEEFKREFGEHTKMTDVKPKVMTLGTSLDRQPA 540
QY 541 ELHLFRNYDAPETVREPQNQVNLPPAQPDSQDLVWRAARSSGAAPTFRPNRFLDGG 600
DB 541 ELHLFRNYDAPEVIREPQNINLKPTQPADQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIIVSLGTGRSPQVPTCYDVPFRPSNP 660
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIIVSLGTGRSPQVPTCYDVPFRPSNP 660

RESULT 12
US-09-519-223-2
Sequence 2, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

```

QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
DB 301 RMLLKRGCDVSDTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
QY 361 DNVEMLKALVFGAEVDTPNDGFTPTFLASKIGRQLODLMIHSRARKPAFILGSRDEK 420
DB 361 DNMEMIKALVFGAEVDTPNDGFTPTAFMAKISKQLODLMPISRARKPAFILSSMRDEK 420
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
DB 421 RIHDHLCLDGGVGKGLVIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMVFRMKDEVRGSRPYESGPLEEFKREFGHTKMTDVRKPKVMLTGTLSRQPA 540
DB 481 AYMRGVYFRMKDEVRGSRPYESGPLEEFKREFGHTKMTDVKKPKVMLTGTLSRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQNLPPAOPSQOLVWRAARSSGAAPTYFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPRFNQNLPPAOPSQOLVWRAARSSGAAPTYFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDFRPSNP 660
DB 601 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 10

US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735, 716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 91.4%; Score 3315; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSVTVLNSPPFVKVAVADYTSRVRREEGQLILFONTPNRTWCVLV 60
DB 1 MQFFGLVNTSSVTNLNSPPFVKRISVADYTSHERVREEGQLILFONASNRTWDCILV 60
QY 61 NPNRSGRFLFOLEADALVNFHOVSSOLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120
DB 61 SPNPHSGRFLFOLEADALVNFQFSSQLPFYESSQVLHVEVLQHLSDLIRHPW 120
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKGDSILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRCFHHSRIISCANSTENBEGCTPLHLACRKGDSILVELVQYCHAQMD 180

QY 181 VTDKGETVFHYAVQGDNSOVQLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAFHYAVQGDNSOVQLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARNINMGPNPYTHSAMKFSQKCAEMIISMDSQIHSKOPRYGASPLHWAKNAEMA 300
DB 241 LCNARNCNWGPSPFFIHTAMKFSQKCAEMIISMDSQIHSKOPRYGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
DB 301 RMLLKRGCDVSDTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGNTPHLHLSK 360
QY 361 DNVEMLKALVFGAEVDTPNDGFTPTFLASKIGRQLODLMIHSRARKPAFILGSRDEK 420
DB 361 DNMEMIKALVFGAEVDTPNDGFTPTAFMAKISKQLODLMPISRARKPAFILSSMRDEK 420
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
DB 421 RIHDHLCLDGGVGKGLVIIQLLIAIEKASGVATKOLFVWAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMVFRMKDEVRGSRPYESGPLEEFKREFGHTKMTDVRKPKVMLTGTLSRQPA 540
DB 481 AYMRGVYFRMKDEVRGSRPYESGPLEEFKREFGHTKMTDVKKPKVMLTGTLSRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQNLPPAOPSQOLVWRAARSSGAAPTYFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPRFNQNLPPAOPSQOLVWRAARSSGAAPTYFRPNRFLDGG 600
QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDFRPSNP 660
DB 601 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 11

US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid

QY	547	NYDAPETVREPRFNQVNLRRPAPQSPDQVWRAARSSGAAPTFRPNNGRFLDGLLANNP	606
DB	614	NYDAPETVREPRFNQVNLRRPAPQSPDQVWRAARSSGAAPTFRPNNGRFLDGLLANNP	673
QY	607	TLDAMTEIHEYNDLIRGOANKYKLSIVVSLGTGRSPQVPTCVDFRPPSPNWEAKT	666
DB	674	TLDAMTEIHEYNDLIRGOANKYKLSIVVSLGTGRSPQVPTCVDFRPPSPNWEAKT	733
QY	667	VFGAKELGKVVVDDCCTDPDGR	687
DB	734	VFGAKELGKVVVDDCCTDPDGR	754
RESULT 8			
US-08-281-193-2			
; Sequence 2, Application US/082811193			
; Patent No. 5466595			
; GENERAL INFORMATION:			
; APPLICANT: Jones, Simon			
; APPLICANT: Tang, Jim			
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B			
; NUMBER OF SEQUENCES: 15			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/281.193			
; FILING DATE:			
; CLASSIFICATION: 435			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 752 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-281-193-2			
Query Match 91.4%; Score 3315; DB 1; Length 752;			
Best Local Similarity 90.4%; Pred. No. 0;			
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0			
QY	1	MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDVRBEGQLILFQNTPNRTWDCVLV	60
DB	1	MOFFGRLVNTLSSVTNLFSNPRVKEISVADYTSHERVREBQILLFQNASNETWDCILV	60
QY	61	NPRNSOGRLFOLELEADALVNFHQYSSQLLPYESSQVVLHTEVLQHTDLIRNHPSW	120
DB	61	SPRNPHSGRLFOLESEADALVNFQFSSQLPPFYESSVQVLHVEVLQHLSDLIRSHPSW	120
QY	121	SVAHLAVELGIRECFPHSRILISCANCAENEGCTPLHLACRKGDETLVELVOYCHTQMD	180
DB	121	TVTHLAVELGIRECFPHSRILISCANSTENEGCTPLHLACRKGDETLVELVOYCHQAMD	180
QY	181	VTDYKGETVFHYAVQGDNSQVLLGLGRNAVAGLNVQNNQGLTPLHLACQLGKQEMVRVLL	240
DB	181	VTDNKGETAFHYAVQGDNSQVLLGLGNASAGLNVQNNQGLTPLHLACQKQEMVRVLL	240
QY	241	LCNARCININGPGNYPIHSHAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA	300
DB	241	LCNARCINVMGSPGFPIHTAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA	300
QY	301	RMLLKGCNVNSTSSNAGNTALHGVYMRNRFDCATVLLTHGANADARGEHNTPLHLAMSK	360
DB	301	RMLLKGCVDVDSAGNTALHVAVMNRNRFDCVWVLLTYGANAGTPEGEHNTPLHLAISK	360
QY	361	DNVEMIKALIVFGAEVDTPNDPGETPTFLASKIGROLQDLMIHISRAKPAFILGSMRDEK	420
DB	361	DNVEMIKALIVFGAEVDTPNDPGETPTFAWSKISKQLQDLMPISRAKPAFILSSMRDEK	420
QY	421	RTHDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKOLFDFWAGVSTGTGGIILALAILHKSMM	480

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Db      421  |RIHHLLCLDGGGVKGLV|IIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKS|SM 480
Qy      481  |AYRMGYFMKDEVFGRSGRPY|ESGPLEEF|LKRFEFGHTKMTDVRKPKVMLTGTLSDRQPA 540
Db      481  |AYRMGYFMKDEVFGRSGRPY|ESGPLEEF|LKRFEFGHTKMTDVRKPKVMLTGTLSDRQPA 540
Qy      541  |ELHLFNYDAPETVRPRFRNQ|NVNLPAPQPSQDLVWRAARSSGAAPTYFRPNGRFLDGG 600
Db      541  |ELHLFNYDAPEVIREFRFNQ|NINLKPPTQPADQLVWRAARSSGAAPTYFRPNGRFLDGG 600
Qy      601  |LLANNPTLDAWTEIHEYND|LIRKGQANKVKKLSIVVSLGTGRSSPOVPVTCVDVFRPSNP 660
Db      601  |LLANNPTLDAWTEIHEYND|LMIRKQGNKVKKLSIVVSLGTGRSSPOVPVTCVDVFRPSNP 660
Qy      661  |WELAKTVFGAKELGKMV|VDCCTDPDGR 687
Db      661  |WELAKTVFGAKELGKMV|VDCCTDPDGR 687

RESULT 9
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match          91.4%; Score 3315; DB 1; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 33; Mismatches 34; Indels 0; Gaps 0;

Qy      1  |MQPFGRLVNTFSGVTN|LFSNPFVRKEVAVADYTSDDVRBEGQLILFQNTPNRTWDCVLV 60
Db      1  |MQPFGRLVNTLSSVTN|LFSNPFVRKEISVADYTSHERVBEGQLILFQNASNRTWDCILV 60
Qy      61  |NPRNSGGFLFOLE|EADALVNPHQVSSQLLPFYESSPOVLHTEVLOHLTDLIRNHPSW 120
Db      61  |SPRNPHSGFLFOLE|SEADALVNFPQPSQLPPFYESSVOLHVEVLQHLSDLIRSHPSW 120
Qy      121  |SVAHLAVELGIRCE|FHHSRIISCANCAENEGCTPLHLACRKGDETLVELVOYCHTQMD 180
Db      121  |TVTHLAVELGIRCE|FHHSRIISCANSTENEGCTPLHLACRKGDETLVELVQYCHAQMD 180
Qy      181  |VTDYKGTVPFHYA|VQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db      181  |VTDNKGETA|PHYAVQGDNSQVLQLLKGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
Qy      241  |LCNARNCMGPN|GYPHTSAWKFSQKQCAEMIISMDSSQIHSKDPRYCASPLHWAQNAEMA 300
Db      241  |LCNARNCMVPS|GFPHTAMKFSQKQCAEMIISMDSSQIHSKDPRYCASPLHWAQNAEMA 300

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 99.5%; Score 3606.5; DB 4; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLELEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLELEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTDLIRNHPWS 120
QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 180
DB 121 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDGSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDGSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIINGPYTHSANKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIINGPYTHSANKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
QY 421 RTHDHLCLDGGVKGILIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMM 480
DB 420 RTHDHLCLDGGVKGILIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMM 479
QY 481 AYMRGMVFRMKDVRFGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
DB 480 AYMRGMVFRMKDVRFGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSQVLVRAARSGGAAPTYFRPNRGFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSQVLVRAARSGGAAPTYFRPNRGFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659

QY 661 WELAKTVFGAKELGKGMVVDCCDTPDGRP 688
DB 660 WELAKTVFGAKELGKGMVVDCCDTPDGRP 687
RESULT 7
US-09-949-016-10948
Sequence 10948, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10948
LENGTH: 819
TYPE: PRT
ORGANISM: Human
US-09-949-016-10948

Query Match 98.5%; Score 3572; DB 4; Length 819;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;
QY 1 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 14 MQFFGRLVNTFSGVTNLFNSNPFVRKVEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 73
QY 61 NPNRSQSGRLFOLELEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTDLIRNHPWS 120
DB 74 NPNRSQSGRLFOLELEADALVNFHQSOLLPPFYESSQVLHTEVLOHLTDLIRNHPWS 133
QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 180
DB 134 SVAHLAVALGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDDGILVELVOYCHTQMD 193
QY 181 VTDYKGETVFHYAVQDGSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 194 VTDYKGETVFHYAVQDGSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 253
QY 241 LCNARCNIINGPYTHSANKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 254 LCNARCNIINGPYTHSANKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 313
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 314 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 373
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGR----- 395
DB 374 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRLVTRKAILTLRTVGAECYCFPIHG 433
QY 396 -----OLQDLMIHSRARKPAFILGSMRDEKRTDHL 426
DB 434 VPAEQSSAAHPHPSLERAQPPPISLNNLEQLQDLMIHSRARKPAFILGSMRDEKRTDHL 493
QY 427 LCLDGGVKGILIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMMAYRGM 486
DB 494 LCLDGGVKGILIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMMAYRGM 553
QY 487 YFRMKDEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 546
DB 554 YFRMKDEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 613

QY 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAENA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAENA 300
QY 301 RMLLKRCNCNVSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCNCNVSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
QY 421 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 480
DB 420 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 479
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
DB 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCVDVFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCVDVFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDDPGRP 688
DB 660 WELAKTVFGAKELGKMWVDCCTDDPGRP 687

RESULT 5

US-09-519-223-21
; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-519-223-21
Query Match 99.5%; Score 3606.5; DB 3; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
QY 61 NFRNSQSQRFLQFLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHQLTLIRNHPSW 120
DB 61 NFRNSQSQRFLQFLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHQLTLIRNHPSW 120
QY 121 SVAHLAVALGIRECPHHHSRIISCANCAENEGECTPLHLACRKGDEGILVELVOYCHTQMD 180
DB 121 SVAHLAVALGIRECPHHHSRIISCANCAENEGECTPLHLACRKGDEGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHVAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHVAVOGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAENA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHAKNAENA 300
QY 301 RMLLKRCNCNVSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCNCNVSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
QY 421 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 480
DB 420 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWAGTSGGILALAILHLSKSM 479
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
DB 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDQVWRAARSSGAAPTFRPNRFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCVDVFRPSNP 660
DB 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKKLSIVVSLGTGRSPQVPTCVDVFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDDPGRP 688
DB 660 WELAKTVFGAKELGKMWVDCCTDDPGRP 687

RESULT 6

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

QY	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQDLVWEAARSSGAAPTYFRPNCGRFLDGG	600
Db	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQDLVWEAARSSGAAPTYFRPNCGRFLDGG	600
QY	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP	660
Db	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP	660
QY	661	WELAKTVFGAKELGKMWVDDCCTDDPDRP	688
Db	661	WELAKTVFGAKELGKMWVDDCCTDDPDRP	688
RESULT 4			
US-08-555-568B-21			
; Sequence 21, Application US/085555568B			
; Patent No. 5976854			
; GENERAL INFORMATION:			
; APPLICANT: Jones, Simon			
; APPLICANT: Tang, Jim			
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B			
; NUMBER OF SEQUENCES: 25			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Genetics Institute, Inc.			
; STREET: 87 CambridgePark Drive			
; CITY: Cambridge			
; STATE: Massachusetts			
; COUNTRY: U.S.A.			
; ZIP: 02140			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/555,568B			
; FILING DATE:			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Brown, Scott A.			
; REGISTRATION NUMBER: 32,724			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617) 498-8224			
; TELEFAX: (617) 876-5851			
; INFORMATION FOR SEQ ID NO: 21:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 688 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-555-568B-21			
Query Match 99.5%; Score 3606.5; DB 2; Length 687;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;			
QY	1	MOFFGRLVNTFSGVTLNLSNPFPRKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
Db	1	MOFFGRLVNTFSGVTLNLSNPFPRKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
QY	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
Db	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD	180
Db	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD	180
QY	181	VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
Db	181	VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
US-09-927-180-23			
Query Match 100.0%; Score 3625; DB 4; Length 688;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MOFFGRLVNTFSGVTLNLSNPFPRKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
Db	1	MOFFGRLVNTFSGVTLNLSNPFPRKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
QY	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
Db	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD	180
Db	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD	180
QY	181	VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
Db	181	VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
QY	241	LCNARNCINMGPGYPHISAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA	300
Db	241	LCNARNCINMGPGYPHISAMKFSQKCAEMIISMDSSQIHSDKDPYRGASPLHWAKNAEMA	300
QY	301	RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGHGNTPPLHLAMSK	360
Db	301	RMLLKRCGNVNTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGHGNTPPLHLAMSK	360
QY	361	DNVEMIKALIVGAEDVTNDPFGTPTFLASIKRQLODLMIHISPAKPAFILGSMRDEK	420
Db	361	DNVEMIKALIVGAEDVTNDPFGTPTFLASIKRQLODLMIHISPAKPAFILGSMRDEK	420
QY	421	RTHDHLCLDGGVGKGLIIQLLIAIERKASGVATKDLFDWVAGTSTGGILALAILHKSMM	480
Db	421	RTHDHLCLDGGVGKGLIIQLLIAIERKASGVATKDLFDWVAGTSTGGILALAILHKSMM	480
QY	481	AYNRGMVFRMKDEVFRGSPYSGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA	540
Db	481	AYNRGMVFRMKDEVFRGSPYSGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA	540

QY	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSSDQLVWEAARSSGAAPTYFRPNCGRFLDGG	600
Db	541	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSSDQLVWEAARSSGAAPTYFRPNCGRFLDGG	600
QY	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP	660
Db	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNP	660
QY	661	WELAKTVFGAKELGKMWVDDCCTDDPDRP	688
Db	661	WELAKTVFGAKELGKMWVDDCCTDDPDRP	688
RESULT 4			
US-08-555-568B-21			
; Sequence 21, Application US/08555568B			
; Patent No. 5976854			
; GENERAL INFORMATION:			
; APPLICANT: Jones, Simon			
; APPLICANT: Tang, Jim			
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B			
; NUMBER OF SEQUENCES: 25			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Genetics Institute, Inc.			
; STREET: 87 CambridgePark Drive			
; CITY: Cambridge			
; STATE: Massachusetts			
; COUNTRY: U.S.A.			
; ZIP: 02140			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/555,568B			
; FILING DATE:			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Brown, Scott A.			
; REGISTRATION NUMBER: 32,724			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617) 498-8224			
; TELEFAX: (617) 876-5851			
; INFORMATION FOR SEQ ID NO: 21:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 688 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-555-568B-21			
Query Match 99.5%; Score 3606.5; DB 2; Length 687;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;			
QY	1	MOFFGRLVNTFSGVTLNLSNPFPRVKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
Db	1	MOFFGRLVNTFSGVTLNLSNPFPRVKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
QY	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
Db	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD	180
Db	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD	180
QY	181	VTDYKGETVFFHVAQVGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
Db	181	VTDYKGETVFFHVAQVGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
US-09-927-180-23			
Query Match 100.0%; Score 3625; DB 4; Length 688;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	MOFFGRLVNTFSGVTLNLSNPFPRVKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
Db	1	MOFFGRLVNTFSGVTLNLSNPFPRVKEVAVADYTSDDRVREGQLILFONTPNRTWDCVLY	60
QY	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
Db	61	NPNRSQSGFRLQLEADALVNFHQSOLLPFYESSPQVLHTEVLOHLDLIRNHPWS	120
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD	180
Db	121	SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEILVELVQYCHTQMD	180
QY	181	VTDYKGETVFFHVAQVGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
Db	181	VTDYKGETVFFHVAQVGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL	240
QY	241	LCNARNCINMGPGYPHISAMKFSQKGCBAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA	300
Db	241	LCNARNCINMGPGYPHISAMKFSQKGCBAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA	300
QY	301	RMLLKRCGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPPLHLAMSK	360
Db	301	RMLLKRCGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPPLHLAMSK	360
QY	361	DNVEMIKALIVGAEDVTNDGFTPTFLASKIGRQLQDLMIHISARKPAFILGSMRDEK	420
Db	361	DNVEMIKALIVGAEDVTNDGFTPTFLASKIGRQLQDLMIHISARKPAFILGSMRDEK	420
QY	421	RTHDHLCLDGGGVKGLIIIIQLLIAIERKASGVATKDLFDWVAGTSTGGILALAILHKSMM	480
Db	421	RTHDHLCLDGGGVKGLIIIIQLLIAIERKASGVATKDLFDWVAGTSTGGILALAILHKSMM	480
QY	481	AYNRMGYFRMKDEVPFRGSPYSGPLEEFLKREFGCHTQMDTVDRKPKVMLTGTLSDRQPA	540
Db	481	AYNRMGYFRMKDEVPFRGSPYSGPLEEFLKREFGCHTQMDTVDRKPKVMLTGTLSDRQPA	540

QY 121 SVAHLAVELGIRECFHSHSRIISCAENCAENBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHSRIISCAENCAENBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLOQLMHI SRARKPAF ILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLOQLMHI SRARKPAF ILGSMRDEK 420
QY 421 RTHDHLCLDGGVKGKGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
DB 421 RTHDHLCLDGGVKGKGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSDRQPA 540
DB 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMTLGTLSDRQPA 540
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DB 541 ELHLFRNYDAPETVREPRFNQVNLPPAQPDSQLVWRAARSSGAAPTFRPGRFLDGG 600
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DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSI VVSLGTGRSPQVPTCVDFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDDCCTDPDGRP 688
DB 661 WELAKTVFGAKELGKMWVDDCCTDPDGRP 688

RESULT 2

US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8824
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-23

Query Match 100.0%; Score 3625; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOFFGRLVNTSGVTNLFSPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
DB 1 MOFFGRLVNTSGVTNLFSPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
QY 61 NPNRSQSGFRLLFQLEADALVNFHOYSSQLLPFYESSPQVLHTEVQLHLTDLIRNHPSM 120
DB 61 NPNRSQSGFRLLFQLEADALVNFHOYSSQLLPFYESSPQVLHTEVQLHLTDLIRNHPSM 120
QY 121 SVAHLAVELGIRECFHSHSRIISCAENCAENBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHSRIISCAENCAENBEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQEMVRVLL 240
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DB 241 LCNARCNIMGPNGYPIHSAMKFSQKGAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLOQLMHI SRARKPAF ILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLOQLMHI SRARKPAF ILGSMRDEK 420
QY 421 RTHDHLCLDGGVKGKGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
DB 421 RTHDHLCLDGGVKGKGLIIIIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSM 480
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DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSI VVSLGTGRSPQVPTCVDFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDDCCTDPDGRP 688
DB 661 WELAKTVFGAKELGKMWVDDCCTDPDGRP 688

RESULT 3

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 25.3702 Seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfilees1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3625	100.0	688	3	US-09-519-223-23
3	3625	100.0	688	4	US-09-519-223-23
4	3606.5	99.5	687	2	US-09-519-223-21
5	3606.5	99.5	687	3	US-08-555-568B-21
6	3606.5	99.5	687	4	US-09-519-223-21
7	3572	98.5	819	4	US-09-519-223-21
8	3315	91.4	752	1	US-09-519-223-2
9	3315	91.4	752	1	US-08-422-106-2
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11	3315	91.4	752	2	US-08-555-568B-2
12	3315	91.4	752	3	US-09-519-223-2
13	3315	91.4	752	4	US-09-519-223-2
14	3315	91.4	752	5	PCT-US95-08069-2
15	2084	57.5	394	2	US-08-555-568B-17
16	2084	57.5	394	3	US-09-519-223-17
17	2084	57.5	394	4	US-09-519-223-17
18	1531	42.2	292	2	US-08-555-568B-19
19	1531	42.2	292	3	US-09-519-223-19
20	1531	42.2	292	4	US-09-519-223-19
21	1165	32.1	896	4	US-09-270-767-46130
22	904	24.9	545	4	US-09-270-767-61684
23	371	10.2	143	4	US-09-270-767-33298
24	338	9.3	843	2	US-09-172-977-3
25	338	9.3	843	4	US-09-404-108-3
26	332	9.2	1839	2	US-09-172-977-4
27	332	9.2	1839	4	US-09-404-108-4

28	332	9.2	2753	4	US-09-949-016-7659	Sequence 7659, Ap
29	332	9.2	2753	4	US-09-949-016-7660	Sequence 7660, Ap
30	332	9.2	3924	4	US-09-538-092-1246	Sequence 1246, Ap
31	308.5	8.5	1745	2	US-09-031-485-33	Sequence 33, Appl
32	308.5	8.5	1745	2	US-08-847-429A-33	Sequence 33, Appl
33	308.5	8.5	1745	3	US-09-065-474-33	Sequence 33, Appl
34	308.5	8.5	1745	3	US-09-557-034-33	Sequence 33, Appl
35	301.5	8.3	786	4	US-09-509-802-2	Sequence 2, Appli
36	301.5	8.3	787	3	US-09-188-930-334	Sequence 334, App
37	301.5	8.3	787	4	US-09-312-283C-334	Sequence 334, App
38	236	8.2	1088	3	US-09-082-059-2	Sequence 2, Appli
39	236	8.2	3913	4	US-09-949-016-10933	Sequence 10933, A
40	236	8.2	4377	4	US-09-949-016-6978	Sequence 6978, Ap
41	294	8.1	1719	4	US-09-949-016-6966	Sequence 6966, Ap
42	294	8.1	1856	4	US-09-949-016-6964	Sequence 6964, Ap
43	294	8.1	1880	4	US-09-949-016-5876	Sequence 5876, Ap
44	294	8.1	1881	4	US-09-949-016-6965	Sequence 6965, Ap
45	294	8.1	1883	4	US-09-949-016-9010	Sequence 9010, Ap

ALIGNMENTS

RESULT 1
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-23

Query Match	100.0%;	Score 3625;	DB 2;	Length 688;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 688;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQFFGRLVNTFSGVTNLFSPNPFVKVAVADYTSRVRREGQLILFQNTPNRTWDCVLV	60	
Db	1	MQFFGRLVNTFSGVTNLFSPNPFVKVAVADYTSRVRREGQLILFQNTPNRTWDCVLV	60	
Qy	61	NPRNSQSGFRLFOLELEADALVNFHOYSQQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW	120	
Db	61	NPRNSQSGFRLFOLELEADALVNFHOYSQQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW	120	

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Job time : 95.803 secs

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; Publication No. US20030104482A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virga, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
; TITLE OF INVENTION: (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/10/299,327
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/509,802
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-299-327-2

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD--SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ--GDNQSVQLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLLARKTSVNKXDEQDWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNIMGNGY--PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDWALPLHYAAWQGHLPVTKLLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILIDLCSDVNICSLQAQTPPLHVAETGHTSTARLLHHRGAGEAL 668
QY 314 SSAGNTALHVGVMNRFPDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHGLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDTPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ--GRHSQ 751

RESULT 14
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US200301099462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD--SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ--GDNQSVQLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLLARKTSVNKXDEQDWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNIMGNGY--PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDWALPLHYAAWQGHLPVTKLLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILIDLCSDVNICSLQAQTPPLHVAETGHTSTARLLHHRGAGEAL 668
QY 314 SSAGNTALHVGVMNRFPDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHGLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDTPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ--GRHSQ 751

RESULT 15
US-10-128-174-31
; Sequence 31, Application US/10128174
; Publication No. US200301099462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 31
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-31

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD--SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ--GDNQSVQLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLLARKTSVNKXDEQDWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNIMGNGY--PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDWALPLHYAAWQGHLPVTKLLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILIDLCSDVNICSLQAQTPPLHVAETGHTSTARLLHHRGAGEAL 668
QY 314 SSAGNTALHVGVMNRFPDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHGLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDTPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ--GRHSQ 751

Search completed: May 26, 2005, 14:51:08
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; Publication No. US20030104482A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: Bird, Timothy
; APPLICANT: Virga, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
; TITLE OF INVENTION: (DAKAR)
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/10/299,327
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/509,802
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-299-327-2

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD--SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVQYCHTQMDVTDYKGETVFHYAVQ--GDNQSVQLQLGRNAVAGLNQVNNQGLTPLHLACQ 229
DB 491 LLLARKTSVNKXDEQDWTALHFAAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548
QY 230 LKQEMVRVLLCNARCNIMGNGY--PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
DB 549 HGOENIVRTLRRGVGVGLQGDWALPLHYAAWQGHLPVTKLLAKQPGVSVNAQTLDGRT 608
QY 284 PRYGA-----SPLHWAK---NAEMARMLLKRCGNVNST 313
DB 609 PLHLAAQRGHYRVARILIDLCSDVNICSLQAQTPPLHVAETGHTSTARLLHHRGAGEAL 668
QY 314 SSAGNTALHVGVMNRFPDCAIVLLTHGANADARGHGNTPLHLAMSKDNVEMIKALIVFG 373
DB 669 TSEGYTALHAAQNGHGLATVKLLIEEKADVMARGPLNQTLALHAAARGHSEVVEELV--S 726
QY 374 AE-VDTPNDFGETPTFLASKIGRQLQ 398
DB 727 ADLIDLSDQGLSALHLAAQ--GRHSQ 751

RESULT 14
US-10-128-174-13
; Sequence 13, Application US/10128174
; Publication No. US200301099462A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/10/128,174
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-128-174-13

Query Match      8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12;

QY 112 DLIRNHPWSVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
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Db 469 VDARAREQPTLHIASRLGKTEIVQLLQWMAHPDAATTNRYTPLHIISAREQGVDSASVL 526
Qy 272 ISMDSSQIHSKDPRYGASPLHWAK--NAEMARMILLKRGCCNVNSTSSAGNTALHVGVMEN 328
Db 529 --LEAGAAHSLATKKGFTPLHVAAYKGLSDVAKULLQRRAAADSAGKNGLTPLHVAAHYD 586
Qy 329 RFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPDNDFGFTPTF 388
Db 587 NQKVALLLEKGGASPHATAKNGYTPHLIAAKKNQWQIASTLLINYGAETNIVTKQGVTPPLH 646
Qy 389 LASKIG 394
Db 647 LASQEG 652

RESULT 12
US-10-164-080-2
; Sequence 2, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAB)
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; PRIOR FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-164-080-2

Query Match 8.3%; Score 301.5; DB 14; Length 786;
Best Local Similarity 29.1%; Pred. No. 2e-18;
Matches 95; Conservative 60; Mismatches 124; Indels 47; Gaps 12

Qy 112 DLIRNHPSSWAHLAVELGIRECFPHSHRSIIISCANCAENEGCTPLHLAC-RKGDEILVE 170
Db 434 DLVLD-SSASULLHLAVAGEQECVKWILLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
Qy 171 LVQYCHTQMDVTDYKGTSTVFHYAVQ-GDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQ 229
Db 491 LLLARKTSVNAKEDQDWTALHFAQNGDEASTRLLEKN--ASVNEVDFEGTTPMVAQCQ 548
Qy 230 LGKQEWYRVLLLCNARNINMGNGY-PIHSAMKFSQKCAEMI-----ISMDSQIHSKD 283
Db 549 HGQENIVRTLLRRGVGVGLQKDAWLPLHYAAWQGHLPVVKLLAKQPGVSVNAQTLDGRT 608
Qy 284 PRYCA-----SPLHWAK---NAEMARMILLKRGCCNVNST 313
Db 609 PLHLAAQRGHYRVARILIDLCSDVNICSLQAQTPHLHVAAGTSTARLLLRGAGKEAL 668
Qy 314 SSAGNTALHVGVMENRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFG 373
Db 669 TSGGYTALHAAQNGHLATVKLLIEKADVMDVARGPLNQTLHLAAARGHSEVVVELV--S 726
Qy 374 AE-VDTPNDFGFTPTFLASKIGROLQ 398
Db 727 ADLIDLSDQGLSALHLAAQ-GRHSQ 751

RESULT 13
US-10-299-327-2
; Sequence 2, Application US/10299327

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QY 149 NEEGCTPLHLACRKGDEILVELVOYCHTOMVDYKGETVHYAVQGDNSOVQL--G 206
DB 316 OPEGLSPLMIAVQNTQIETVSMMLDH-GADINILSSEQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGTLPLHLACQLGKQEMVRVLLLCNARCNIWGPNG-----Y 254
DB 375 KKCETMIQNTDSNGTYPAYVA-----LINACLSNCQTLRGFGGGIQQSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSQIHSKDPYRGASPLHAKNAEMAMLLKR---GCN 309
DB 425 PIIGAMKRGKLDVSLRKMLKQDGLTETPTTGNVTIHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVKDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTIARML 544
QY 370 IVFGAEVDPNDPFGTPTFLASKI-----LLCLDGGVKGKLIILIIOLIAIEKASGVATKDL 457
DB 665 FPHEALRVKRNKELVEKKTSNVINVLGDDGGIRGLVTQVQLICLAEFLDRPLIDY 724
QY 458 FOWAGTSTGGILALAILHSKSMAYMRGMYPFMKDEVFGR-SRPYESGPLEBFLKREGE 516
DB 725 FDMIGATSGCYIMSTMGTGSLRKAQRYLMFKQDLFDSWTRPYDTKTLETTFIORAFA 784
QY 517 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQILV 576
DB 785 DRLMGDIKYPFFCTTVRADTFPVQLELLRNRLPISEKE---NNDLGF---TDPNELTI 838
QY 577 WRAARSSGAAPTYFRPN-GRFLDGLLANNPTLDAMTEIHEYNQDLIRKGQANKVKLSI 635
DB 839 WKATRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKMRIPERKVMVMGMC 898
QY 636 VVSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMVVDCTDPDGRP 688
DB 899 VLSVGTGITPICVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATEGAP 947

RESULT 9
US-10-369-493-6690
; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6690
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6690

Query Match 17.3%; Score 627; DB 15; Length 1023;
Best Local Similarity 23.9%; Pred. No. 1.5e-48;
Matches 185; Conservative 153; Mismatches 285; Indels 150; Gaps 23;

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QY 37 RVREBQILILFQNTPNRTWDCVILVNPRNSQSGFRFLQLELEAD--ALVNFHOYSQILPFP 94
DB 204 RAKEEEL---KNRPLYHLAITLYNENNEKYVMSLFRSHKLDVVALCERCERENPELPRV 260
QY 95 YESSPOV---LHTEVLQHLTDLIRNHPWSVAHLAVELGIRECFPH---SRIISCANCAE 148
DB 261 PPKVNIKDYLHT-----IFHELDRNMTWKSVHISKIGLLEYFENMEKHLKKYLNLIV 315
QY 149 NEEGCTPLHLACRKGDEILVELVOYCHTOMVDYKGETVHYAVQGDNSOVQL--G 206
DB 316 OPEGLSPLMIAVQNTQIETVSMMLDH-GADINILSSEQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGTLPLHLACQLGKQEMVRVLLLCNARCNIWGPNG-----Y 254
DB 375 KKCETMIQNTDSNGTYPAYVA-----LINACLSNCQTLRGFGGGIQQSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSQIHSKDPYRGASPLHAKNAEMAMLLKR---GCN 309
DB 425 PIIGAMKRGKLDVSLRKMLKQDGLTETPTTGNVTIHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
DB 485 PEARNALQOTPLHTFVKDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTIARML 544
QY 370 IVFGAEVDPNDPFGTPTFLASKI-----LLCLDGGVKGKLIILIIOLIAIEKASGVATKDL 457
DB 665 FPHEALRVKRNKELVEKKTSNVINVLGDDGGIRGLVTQVQLICLAEFLDRPLIDY 724
QY 458 FOWAGTSTGGILALAILHSKSMAYMRGMYPFMKDEVFGR-SRPYESGPLEBFLKREGE 516
DB 725 FDMIGATSGCYIMSTMGTGSLRKAQRYLMFKQDLFDSWTRPYDTKTLETTFIORAFA 784
QY 517 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQILV 576
DB 785 DRLMGDIKYPFFCTTVRADTFPVQLELLRNRLPISEKE---NNDLGF---TDPNELTI 838
QY 577 WRAARSSGAAPTYFRPN-GRFLDGLLANNPTLDAMTEIHEYNQDLIRKGQANKVKLSI 635
DB 839 WKATRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKMRIPERKVMVMGMC 898
QY 636 VVSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMVVDCTDPDGRP 688
DB 899 VLSVGTGITPICVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATEGAP 947

RESULT 10
US-10-369-493-4998
; Sequence 4998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 292 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match      42.2%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.4e-133;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 LQDLMHISRAKPAFILGSRMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 456
Db 1 LQDLMHISRAKPAFILGSRMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60

QY 457 LFDWVAGTSGGILALAILHKSMAVMYRMKDEVRFGSPYSGPLEEFLKEFGE 516
Db 61 LFDWVAGTSGGILALAILHKSMAVMYRMKDEVRFGSPYSGPLEEFLKEFGE 120

QY 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAOPSDQLV 576
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAOPSDQLV 180

QY 577 WRAARSSGAAPTYFRPNRFLDGLGLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV 636
Db 181 WRAARSSGAAPTYFRPNRFLDGLGLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV 240

QY 637 VSLGTRSGPOVPVTCVDVRPSPNPELAKTVFGAKELGKVVDCCTDPPGRP 688
Db 241 VSLGTRSGPOVPVTCVDVRPSPNPELAKTVFGAKELGKVVDCCTDPPGRP 292

RESULT 7
US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6865
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6865

Query Match      18.0%; Score 651; DB 15; Length 1071;
Best Local Similarity 27.1%; Pred. No. 9.2e-51;
Matches 195; Conservative 125; Mismatches 260; Indels 140; Gaps 20;

QY 69 FRLEOLELEADALVNFHVOYSSQLLPVYESSPOVLHTEVL---OHLTDLIRNHPSSVAH 124
Db 315 FSLFRATDKDMLDLHLCDKESFLTSLDMSTMRADILRSKIEELVIQRLKPHYMH 374

QY 125 LAVELGIRECFHRSRI-----ISCANCAENEEGCTPLHLACRKGSGEILVELVOY 174
Db 375 VALATRLDFSDGMKTMNETLEPPESQLRCLCHTENCYVPVHLATMDRQKIVERLLEL 434

QY 175 CHTQMDVTDYKGTVFHYAVQGNDSQVLQLGRNAVAG---LNQVNNQGLTPLHLACQLG 231
Db 435 DPTLFCETDKAGNVVHHV---NSSFCAQIWDRCFASQHFIDERNMDGQSPLEAVSTA 491
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QY 232 KOEMVRVLLLCNARCINMGPNGYPIHSAWKFSQKGAEMIISM-----DSS 277
Db 492 KPLVATFL-----IGKGAFTRGDRNELFVAMTSKNAQSVVEWLTDPK 535

QY 278 QIHSDKPRYGASPLHWAKNAEMARMLLKR---GCNVNSTSSAGNTALHVGVMRNPDC 333
Db 536 EIANERDALGNSAIIHVALYKESINALLNRKVELGDIIDVKNNAGETALLLLFITRKP 595

QY 334 IVLLT---HGANADARGEHNTPLHLAMS-----KONVEMIKALIVFGAEVDTPNDF 385
Db 596 PLIVTLIYAHGANNNATDPGNTALHKSAAVLDAKKSILECVKFLISAGSNPNKINLR 655

QY 386 PTFLASKIGRQLQDLMHISRA---RKPAFILG-----SMRDE----- 419
Db 656 PRHLAASL--NQOEMLAILKAAGATRCPKGYKGRSNCRHRDCSSAEDEYEETLQKIR 713

QY 420 -----KATHDHLCLDGGGVKGLIIQLLIAIEKASGV 452
Db 714 ESDYEKTEFTASEKLNIOPTLDGSRGKAKKVNLIISMGGGIRGLVIIQTLIAIEB 773

QY 453 ATKDLFDWVAGTSGGILALAILHKSMAVMYRMKDEVRFG--SRPYESGPLEEFLK 511
Db 774 DIFKTFDWSAGTSGSLMAGLATGKSLREMOQTYLLDKORVDFDGMPPDITVQLSE 833

QY 512 REFGEHTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPP 571
Db 834 DQFGTGT-VWEIPEPLMISAVNSEKL PVRLEMARNYKPAKV-----APETP 880

QY 572 SQDLVWRAARSSGAAPTYFRPN--GRFLDGLGLANNPTLDAMTEIHEYNQDLIRKGO 630
Db 881 KEMPLMALLRSTAAAPVLPKPSEDRYIDGGIISNNPALDLMSEVHAYNRELQLSGRK 940

QY 631 KKLSTVSLGTRSGPOVPVTCVDVFR--PSNPWELAKTVFGAKELGKVVDCCTDPP 688
Db 941 VQNVLVSPGTG---QIPSTVIETLSIDNSPLQSIKTI---KNLAAMFIDQATASEG 994

RESULT 8
US-10-369-493-6689
; Sequence 6689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6689
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6689

Query Match      17.3%; Score 627; DB 15; Length 1023;
Best Local Similarity 23.9%; Pred. No. 1.5e-48;
Matches 185; Conservative 153; Mismatches 285; Indels 150; Gaps 23;

QY 37 RVRESQLILFQNTNRTWDCVLNPRNSQSGRFLRQLELEAD--ALVNFHVOYSSQLLP 94
Db 204 RAKEEBEL---KNKPLYHLAITLYNENNEKYVMSLFRSHKLADVVALCERCENPEL 260

QY 95 YESSPOV---LHTEVLQHLTDLIRNHPSSVAHLAVELGIRECFH---SRISCANCA 148
Db 261 FPKNVNIDKYLHT-----IFHELNDNTWKSVHISKIGLLEYFENMKHKLKYLNL 315
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Db 102 LCNARCNMGNGYPIYSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 161
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGTPLHLAMSK 360
Db 162 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGTPLHLAMSK 221
QY 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGR-----QLQDLMHISRAKPAFTLGSMRDEKTHDL 426
Db 222 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIGR-----QLQDLMHISRAKPAFTLGSMRDEKTHDL 281
QY 396 -----QLQDLMHISRAKPAFTLGSMRDEKTHDL 426
Db 282 VPAEQGSRAHPHPSLERAQPPISINLLEQLDLMHISRAKPAFTLGSMRDEKTHDL 341
QY 427 LCLDGGVKGIIIIQLLIAEKASGATKDLFDWVAGTSTGGILAILHLSKSMAYMRGM 486
Db 342 LCLDGGVKGIIIIQLLIAEKASGATKDLFDWVAGTSTGGILAILHLSKSMAYMRGM 401
QY 487 YFRMKDEVPRGSRPYESGPLEFLKREGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 546
Db 402 YFRMKDEVPRGSRPYESGPLEFLKREGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 461
QY 547 NYDAPETVREPFRNQVNLPRPAQPSDQLVWRAARSSGAAPYFRPNRGFRFLDGGILLANP 606
Db 462 NYDAPETVREPFRNQVNLPRPAQPSDQLVWRAARSSGAAPYFRPNRGFRFLDGGILLANP 521
QY 607 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 666
Db 522 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT 581
QY 667 VFGAKELGMVYDCCDDPGR 687
Db 582 VFGAKELGMVYDCCDDPGR 602

RESULT 5
US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17
Query Match 57.5%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 7.4e-185; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;
QY 1 MQFFGRLVNTSGVTNLFSPNFRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVILV 60
Db 1 MQFFGRLVNTSGVTNLFSPNFRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVILV 60
QY 61 NPNRSQSGFRILFOLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW 120
Db 61 NPNRSQSGFRILFOLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIG 394
Db 361 DNVEIMKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 6
US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid

Query Match	91.4%;	Score 3315;	DB 9;	Length 752;
Best Local Similarity	90.4%;	Pred. No. 5e-299;		
Matches 621;	Conservative 32;	Mismatches 34;	Indels 0;	Gaps 0
Qy	1	MOFFGRLVNTSGVTNLSFNPFRVKEVAVADYTSSDRVEGQLILFQNTNRTWDCVIL	60	
Db	1	MOFFGRLVNTLSSVTNLSFNPFRVKEISVADYTSHERVREGQLILFQNASNRTWDCILV	60	
Qy	61	NPRNSQSGFRILFOLEADALVNPHOYSQQLPPFYESSPOVLHTEVLQHLTDLIRNHPSW	120	
Db	61	SPRNPHSGFRILFOLESEADALVNFOQSQQLPPFYESSVOVLHVEVLQHLSDLIRNHPSW	120	
Qy	121	SVAHLAVELGIRECPHHGRILISCANCAENNEECTPLHLACRKGDSIILVELVQYCHTQMD	180	
Db	121	TVTHLAVELGIRECPHHGRILISCANSTENEECTPLHLACRKGDSIILVELVQYCHQAQD	180	
Qy	181	VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVNNGILTPLHLACQLGQEMVRVLL	240	
Db	181	VTDNKGETAFHYAVQGDNSQVLQLLGGKNASAGLNVNNGKGLTPLHLACOMGQEMVRVLL	240	

Qy		241	LCNARCNI	GPN	GYP	I	H	S	A	M	K	F	S	Q	K	G	C	A	E	M	I	I	S	M	D	S	S	Q	I	H	S	K	D	P	R	V	G	A	S	P	L	H	A	K	N	A	E	M	A	300								
Db		241	LCNARCNI	VMG	PS	G	P	I	H	T	A	M	K	F	S	Q	K	G	C	A	E	M	I	I	S	M	D	S	S	Q	I	H	S	K	D	P	R	V	G	A	S	P	L	H	A	K	N	A	E	M	A	300						
Qy		301	RMLLKRG	CNV	N	S	S	A	G	N	T	A	L	H	V	G	W	R	N	R	F	D	C	A	I	V	L	L	T	H	C	A	N	A	D	A	R	G	E	H	G	N	T	P	L	H	L	A	M	S	K	360						
Db		301	RMLLKRG	C	V	D	S	T	S	A	A	G	N	T	A	L	H	V	A	V	R	N	R	F	D	C	V	M	V	L	L	T	Y	G	A	N	A	G	T	P	G	E	H	G	N	T	P	L	H	L	A	I	S	K	360			
Qy		361	DNVEMIK	A	L	I	V	F	G	A	E	V	D	T	P	N	D	F	G	E	T	P	T	F	L	A	S	K	I	G	R	O	L	Q	D	L	M	H	I	S	R	A	K	P	A	F	I	L	G	S	M	R	D	E	K	420		
Db		361	DNVEMIK	A	L	I	V	F	G	A	E	V	D	T	P	N	D	F	G	E	T	P	T	F	A	F	M	A	S	K	I	S	K	O	L	Q	D	L	M	P	I	S	R	A	K	P	A	F	I	L	G	S	M	R	D	E	K	420
Qy		421	RTDHLCL	D	G	G	V	K	G	L	I	I	O	L	L	I	A	E	K	A	S	G	V	A	T	K	O	L	F	D	W	A	G	T	S	T	G	G	I	L	A	I	L	H	S	K	S	M	480									
Db		421	RIHDHLL	C	D	G	G	V	K	G	L	I	I	O	L	L	I	A	E	K	A	S	G	V	A	T	K	O	L	F	D	W	A	G	T	S	T	G	G	I	L	A	I	L	H	S	K	S	M	480								
Qy		481	AYMRGYF	R	M	K	D	R	V	F	G	S	R	P	E	S	G	P	L	E	E	F	L	K	R	F	G	B	H	T	K	M	T	D	V	R	K	P	K	M	L	T	G	T	L	S	D	R	O	P	A	540						
Db		481	AYMRGYF	R	M	K	D	R	V	F	G	S	R	P	E	S	G	P	L	E	E	F	L	K	R	F	G	B	H	T	K	M	T	D	V	K	K	P	K	M	L	T	G	T	L	S	D	R	O	P	A	540						
Qy		541	ELHLFRNY	D	A	P	E	T	V	R	P	R	F	N	Q	N	V	N	L	R	P	P	A	Q	S	D	Q	L	V	M	R	A	R	S	S	G	A	A	P	T	Y	F	R	P	N	G	R	F	L	D	G	G	600					
Db		541	ELHLFRNY	D	A	P	E	V	I	R	P	R	F	N	Q	N	I	N	L	K	P	T	Q	P	A	D	Q	L	V	M	R	A	R	S	S	G	A	A	P	T	Y	F	R	P	N	G	R	F	L	D	G	G	600					
Qy		601	LLANNP	T	L	D	A	M	T	E	I	H	Y	N	O	D	L	I	R	K	G	A	N	K	K	L	S	I	V	V	S	L	T	G	R	S	P	Q	V	P	T	C	D	V	F	R	P	S	N	P	660							
Db		601	LLANNP	T	L	D	A	M	T	E	I	H	Y	N	O	D	M	I	R	K	G	N	K	K	L	S	I	V	V	S	L	T	G	R	S	P	Q	V	P	T	C	D	V	F	R	P	S	N	P	660								
Qy		661	WEIAKT	V	F	G	A	K	E	L	G	K	M	V	D	C	T	D	P	D	G	R	6																																			

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; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match      100.0%; Score 3625; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 688; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVNTLFSNPFVRKEVAVADVTSSDRVEEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGLVNTFSGVNTLFSNPFVRKEVAVADVTSSDRVEEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHTDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHOYSQQLLPFYESSQVLHTEVQLHTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEIILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEIILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYKASPLHWAKNAEMA 300
QY 301 RMLLKRCGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLODLMIHSRARKPAFTILGSMRDEK 420
DB 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRQLODLMIHSRARKPAFTILGSMRDEK 420
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
DB 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTMTDVRKPKVMLTGLSDRQPA 540
DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTMTDVRKPKVMLTGLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFFRPNRFLDGG 600
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFFRPNRFLDGG 600

RESULT 2
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 93.803 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQQFGLVNTFGVTLNFSN.....GAKELGKMVVDCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3625	100.0	688	9 US-09-927-180-23	Sequence 23, Appl
2	3606.5	99.5	687	9 US-09-927-180-21	Sequence 21, Appl
3	3315	91.4	752	9 US-09-927-180-2	Sequence 2, Appl
4	2728.5	75.3	667	15 US-10-108-260A-3778	Sequence 3778, Ap
5	2084	57.5	394	9 US-09-927-180-17	Sequence 17, Appl
6	1531	42.2	292	9 US-09-927-180-19	Sequence 19, Appl
7	651	18.0	1071	15 US-10-369-493-6865	Sequence 6865, Ap
8	627	17.3	1023	15 US-10-369-493-6689	Sequence 6689, Ap
9	627	17.3	1023	15 US-10-369-493-6690	Sequence 6690, Ap
10	326	9.0	468	15 US-10-369-493-4988	Sequence 4988, Ap
11	324	8.9	1330	15 US-10-108-260A-3237	Sequence 3237, Ap
12	301.5	8.3	786	14 US-10-164-080-2	Sequence 2, Appl
13	301.5	8.3	786	14 US-10-299-327-2	Sequence 2, Appl

14	301.5	8.3	786	14	US-10-128-174-13	Sequence 13, Appl
15	301.5	8.3	786	14	US-10-128-174-31	Sequence 31, Appl
16	301.5	8.3	786	14	US-10-128-174-32	Sequence 32, Appl
17	301.5	8.3	786	14	US-10-128-174-33	Sequence 33, Appl
18	301.5	8.3	787	10	US-09-866-050A-334	Sequence 334, App
19	301.5	8.3	1724	9	US-09-964-899-43	Sequence 43, Appl
20	301	8.3	347	14	US-10-128-174-30	Sequence 30, Appl
21	296	8.2	1094	17	US-10-479-764-22	Sequence 22, Appl
22	296	8.2	3913	15	US-10-334-143-45	Sequence 45, Appl
23	293.5	8.1	1762	14	US-10-205-194-117	Sequence 117, App
24	286.5	7.9	720	15	US-10-433-794-20	Sequence 20, Appl
25	286.5	7.9	765	14	US-10-128-174-3	Sequence 3, Appl
26	286.5	7.9	765	14	US-10-128-174-34	Sequence 34, Appl
27	286.5	7.9	765	14	US-10-128-174-35	Sequence 35, Appl
28	286.5	7.9	765	14	US-10-128-174-36	Sequence 36, Appl
29	286.5	7.9	765	14	US-10-128-174-37	Sequence 37, Appl
30	286.5	7.9	765	14	US-10-128-174-38	Sequence 38, Appl
31	286.5	7.9	765	14	US-10-128-174-39	Sequence 39, Appl
32	286.5	7.9	765	14	US-10-128-174-40	Sequence 40, Appl
33	286.5	7.9	765	14	US-10-128-174-41	Sequence 41, Appl
34	286.5	7.9	765	14	US-10-128-174-42	Sequence 42, Appl
35	286.5	7.9	765	14	US-10-128-174-43	Sequence 43, Appl
36	286.5	7.9	765	14	US-10-128-174-44	Sequence 44, Appl
37	286.5	7.9	765	15	US-10-182-243-56	Sequence 56, Appl
38	284	7.8	784	14	US-10-164-080-7	Sequence 7, Appl
39	284	7.8	784	15	US-10-258-951-70	Sequence 70, Appl
40	282	7.8	784	14	US-10-354-358-38	Sequence 38, Appl
41	282	7.8	784	14	US-10-128-174-12	Sequence 12, Appl
42	282	7.8	784	15	US-10-658-904-2	Sequence 2, Appl
43	281	7.8	784	16	US-10-648-593-153	Sequence 153, App
44	273	7.5	367	15	US-10-250-613-6	Sequence 6, Appl
45	273	7.5	994	17	US-10-717-665-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:

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Qy	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIIVSLGTGRSPQVPVTCVDVFRPSNP	660
Db	601	LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIIVSLGTGRSPQVPVTCVDVFRPSNP	660
Qy	661	WELAKTVFGAKELGKMVVDCCCTDPDGR	687
Db	661	WELAKTVFGAKELGKMVVDCCCTDPDGR	687

Search completed: May 26, 2005, 14:13:57
Job time : 92.0457 secs

Db 121 TVTHLAVELGIRECPHSHRIISCANSTENEEGCTPLHLACRKGDSSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
Db 181 VTDNKGETAFFHYAVQGDNSQVQLLGNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVMGSPGFPPIHTAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRGCNVDSTSAAGNTALHVAVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIGRQLQDLMIHSRARKPAFILGSRDEK 420
Db 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIGRQLQDLMIHSRARKPAFILGSRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
Db 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFLEKREFEHNTKMTDVRKPKVMTLGTLSDRQPA 540
Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFLEKREFEHNTKMTDVRKPKVMTLGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 601 LIANNPDLTAMTEIHEYNODLIRKGOANKVKLSIVVSLGTGRSPQVPTCVDFRPNRP 660
Db 601 LIANNPDLTAMTEIHEYNODLIRKGOANKVKLSIVVSLGTGRSPQVPTCVDFRPNRP 660
QY 661 WELAKTVFGAKELGKMWVDDCTDPDGR 687
Db 661 WELAKTVFGAKELGKMWVDDCTDPDGR 687

RESULT 15
ABB82215
ID ABB82215 standard; protein; 752 AA.
AC ABB82215;
XX
DT 08-JAN-2003 (first entry)
DE Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).
XX
KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX antiasthmatic.
XX
OS Unidentified.
XX
PN US2002106364-A1.
XX
PD 08-AUG-2002.
PF
XX 09-AUG-2001; 2001US-00927180.
XX
PR 27-JUL-1994; 94US-00281193.
PR 14-APR-1995; 95US-00422106.
PR 14-APR-1995; 95US-00422420.
PR 26-JUN-1995; 95WO-US008069.
PR 08-NOV-1995; 95US-00555568.
PR 09-SEP-1998; 98US-00149988.
PR 06-MAR-2000; 2000US-00519223.
XX
(GEM) GENETICS INST INC.
PA
XX Jones S, Tang J;
PI
XX

WPI: 2002-739923/80.
N-PSDB; ABV73007.
Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
Example 4; Page 10-12; 41pp; English.
The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a cPLA2/B enzyme (clone 9)

Sequence 752 AA;
Query Match 91.4%; Score 3315; DB 5; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

QY 1 MQFFGLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVILV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASRKTWDCILV 60
QY 61 NPNRSQSGFRLEADALVNFHYSQQLLPFFESSPOVLTEVQLHLLTDLIRHPSW 120
Db 61 SPRNPHSGFRLEADALVNFHYSQQLLPFFESSPOVLTEVQLHLLTDLIRHPSW 120
QY 121 SVAHLAVELGIRECPHSHRIISCANCAENEECTPLHLACRKGDSSEILVELVQYCHTOMD 180
Db 121 TVTHLAVELGIRECPHSHRIISCANSTENEECTPLHLACRKGDSSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
Db 181 VTDNKGETAFFHYAVQGDNSQVQLLGNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVMGSPGFPPIHTAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRGCNVDSTSAAGNTALHVAVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIGRQLQDLMIHSRARKPAFILGSRDEK 420
Db 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIGRQLQDLMIHSRARKPAFILGSRDEK 420
QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
Db 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILAILHLSKSM 480
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFLEKREFEHNTKMTDVRKPKVMTLGTLSDRQPA 540
Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEEFLEKREFEHNTKMTDVRKPKVMTLGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600
Db 541 ELHLFRNYDAPETVREPRNQVNNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGG 600

FH	Key	Location/Qualifiers				
FT	Active-site	465				
FT	/note= "mutagenesis of Ser-465 results in loss of activity"					
FT						
FT						
PN	WO9717448-A2.					
XX						
PD	15-MAY-1997.					
XX						
XX	07-NOV-1996; 96WO-US017794.					
XX						
PR	08-NOV-1995; 95US-00555568.					
XX						
PA	(GEMY) GENETICS INST INC.					
XX						
PI	Jones S, Tang J;					
XX						
DR	WPI; 1997-281037/25.					
DR	N-PSDB; AAT68827.					
XX						
XX	Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.					
PT						
XX						
PS	Example 4; Page 33-36; 74pp; English.					
XX						
CC	A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AAT68827) obt'd. from a CHO-DUX cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.)					
XX						
XX						
SQ	Sequence 752 AA;					
Query Match 91.4%; Score 3315; DB 2; Length 752;						
Best Local Similarity 90.4%; Pred. No. 0;						
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;						
QY	1	MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60				
DB	1	MQFFGLVNTLSSVTNLFSPNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60				
QY	61	NPRNSOGRFLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVQLHLDLIRNHPWS 120				
DB	61	SPRPHSGRFLFOLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW 120				
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVQYCHTQMD 180				
DB	121	TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSIILVELVQYCHAQMD 180				
QY	181	VTDTKETVFHYAVQDGNOSVOLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240				
DB	181	VTDNKETAFHYAVQDGNOSVOLQLLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240				
QY	241	LCNARCNIWPGNPGYPIHSAKMSQKCAEMIISMDSQIHSKDPYGCASPLHWAKNAEMA 300				
DB	241	LCNARCNIWPGSGFPPIHTAMKFSQKCAEMIISMDSQIHSKDPYGCASPLHWAKNAEMA 300				
QY	301	RMLLKRCNVNSTSSAGNTALHVGVMNRNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360				
DB	301	RMLLKRCVDVSTISAGNTALHVAVMNRNRFDCVMVLLTYGANAGTGEHNTPLHLAISK 360				
QY	361	DNVEMIKALIVGAEDVTPNDFGETPTFLASKIGRQLQDLMIHSIRARKPAFILGSRMDEK 420				
DB	361	DNMEMIKALIVGAEDVTPNDFGETPAFWASKISKQLQDLMPISIRARKPAFILSSMRDEK 420				
QY	421	RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWAGTSGGILALAILHKS 480				
DB	421	RIHDHLCLDGGVGKGLVLIQLLIAIEKASGVATKDLFDWAGTSGGILALAILHKS 480				
QY	481	AYMRGMYFRMKDQEVFRGSRPYESGPLEEFLKRGFGEHTKMTDVRKPKVMLTGTLSDRQPA 540				
DB	481	AYMRGYFRMKDQEVFRGSRPYESGPLEEFLKRGFGEHTKMTDVKPKVMLTGTLSDRQPA 540				
QY	541	ELHLFRNYDAPETVREPRENQNVNLPAPQSPDQLVRAARSSGAAPTYPFRNGRFLDGG 600				
DB	541	ELHLFRNYDAPETVREPRENQNVNLPAPQSPDQLVRAARSSGAAPTYPFRNGRFLDGG 600				
QY	601	LLANNPFLDAMTETIHEYNDQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660				
DB	601	LLANNPFLDAMTETIHEYNDQDMIRKGGKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660				
QY	661	WELAKTVFGAKELGKMVVDCCCTDPDGR 687				
DB	661	WELAKTVFGAKELGKMVVDCCCTDPDGR 687				
RESULT 14						
AAW81825						
ID	AAW81825 standard; protein; 752 AA.					
XX						
AC	AAW81825;					
XX						
DT	02-FEB-1999 (first entry)					
XX						
DE	Chinese hamster calcium independent cPLA2/B protein.					
KW	Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening; anti-inflammatory; arachidonic acid cascade; chinese hamster.					
XX						
OS	Cricetulus griseus.					
XX						
PN	US5840511-A.					
XX						
PD	24-NOV-1998.					
XX						
PF	23-OCT-1996; 96US-00735716.					
XX						
PR	27-JUL-1994; 94US-00281193.					
PR	14-APR-1995; 95US-00422106.					
XX						
PA	(GEMY) GENETICS INST INC.					
XX						
PI	Tang J, Jones S;					
XX						
DR	WPI; 1999-034032/03.					
DR	N-PSDB; AAV64840.					
XX						
PT	Screening assay for phospholipase inhibitors - using specified phospholipase polypeptide.					
XX						
PS	Claim 1b; Col 21-24; 24pp; English.					
XX						
CC	This sequence represents a novel calcium independent cytosolic phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This protein can be used for screening unknown compounds for anti-inflammatory activity mediated by the arachidonic acid cascade					
XX						
SQ	Sequence 752 AA;					
Query Match 91.4%; Score 3315; DB 2; Length 752;						
Best Local Similarity 90.4%; Pred. No. 0;						
Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;						
QY	1	MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60				
DB	1	MQFFGLVNTLSSVTNLFSPNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60				
QY	61	NPRNSOGRFLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVQLHLDLIRNHPWS 120				
DB	61	SPRPHSGRFLFOLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW 120				
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVQYCHTQMD 180				

Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 480

QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540

Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540

QY 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQPDSQDLVWRAARSSGAAPTYFRNGRFLDGG 600

Db 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQPDSQDLVWRAARSSGAAPTYFRNGRFLDGG 600

QY 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

Db 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 12

AAW13163

ID AAW13163 standard; protein; 752 AA.

XX

AC AAW13163;

XX

DT 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

XX

Ca-independent phospholipase A2/B protein.

XX

Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;

KW chromatography; DEAE anion exchange; hydrophobic interaction; lambda;

KW heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;

KW CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.

XX

Cricetulus griseus; ovary cells.

OS

XX

US5589170-A.

PN

XX

31-DEC-1996.

PD

XX

14-APR-1995; 95US-00422106.

PF

XX

27-JUL-1994; 94US-00281193.

PR

XX

(GENY) GENETICS INST INC.

PA

XX

Tang J, Jones S;

PI

XX

WPI; 1997-076789/07.

DR

XX

N-PSDB; AAT59199.

DR

XX

Compen. comprising calcium-independent phospholipase enzyme - for

PT screening for anti-inflammatory agents.

PT

XX

Claim 5; Col 15-22; 24pp; English.

PS

XX

This is the amino acid sequence of the Ca-independent phospholipase A2/B

CC from Chinese hamster ovary cells. The protein was isolated from these

CC cells by conventional chromatographic methods e.g. DEAE anion exchange,

CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20

CC chromatofocusing chromatography. The purified protein has mol. wt. of 86

CC kD and an optimum pH 6. The protein was used for amino acid sequencing

CC from which pools of degenerate probes were synthesised. The probes were

CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 400000

CC recombinant phages screened, 12 positive plaques were isolated. One of

CC these, designated clone 9, contained this sequence. The phospholipase

CC gene can be inserted into eukaryotic vectors for expression in COS or CHO

CC cells. The protein, or peptides derived from it e.g. AAW13164-76, can be

CC used to identify phospholipase inhibitors that can be used as anti-

CC inflammatory agents, esp. against components of the arachidonic acid

CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT

CC -2003 to standardise OS field)

XX

SQ Sequence 752 AA;

Query Match

Best Local Similarity 91.4%; Score 3315; DB 2; Length 752;

Matches 621; Conservative 32; Mismatches 34; Indels 0; Gaps 0;

QY 1 MQFGRVNTSGVTNLFSPNPRVKEVAVADYTSDDRVREBEGQLILPONTNRTWDCVILV 60

Db 1 MQFGRVNTSLSSVTNLFSPNPRVKEIISVADYTSHERVREBEGQLILFONASNRTWDCVILV 60

QY 61 NPNRSQSQFRLLFOLELEADALVNPHOYSSQLLPFYESSQVLHTVEIQLHLDLINHPSW 120

Db 61 SPRNPHSGFRLLFOLESEADALVNFQPSQSPFPFYESSVQVLHVEVQLHSLDIRKPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEIILVELVQYCHTQMD 180

Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEIILVELVQYCHTQMD 180

QY 181 VTDYKGETVPHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACOLQKQEMVRVLL 240

Db 181 VTDNKGETAFAHYAVQGDNSQVLQLLGRKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240

QY 241 LCNARCNIMGNGYPIHSAMKFSQKCAEMIISMDSSQIHSDPRYSGASPLHWAKNAEMA 300

Db 241 LCNARCNVWGSPGPIHTAMKFSQKCAEMIISMDSSQIHSDPRYSGASPLHWAKNAEMA 300

QY 301 RMLLKRCNVNSTSAGNTALHVGVMNRNFDCAIYLLTHGANADARGHGNTPPLHLAMSK 360

Db 301 RMLLKRCGCDVSTSAAGNTALHVAVMNRNFDCAIYLLTHGANADARGHGNTPPLHLAISK 360

QY 361 DNEMIKALIIVFGAEVDPNDFGETPFAWASKISKQLQDLMPISARKPAFTLSSMRDEK 420

Db 361 DNEMIKALIIVFGAEVDPNDFGETPFAWASKISKQLQDLMPISARKPAFTLSSMRDEK 420

QY 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 480

Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 480

QY 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540

Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFGEHTKMTDVRKPKVMTGLTSLDRQPA 540

QY 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQPDSQDLVWRAARSSGAAPTYFRNGRFLDGG 600

Db 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQPDSQDLVWRAARSSGAAPTYFRNGRFLDGG 600

QY 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

Db 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIWSLGTGRSPQVPVTCVDVFRPSNP 660

QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 13

AAW17849

ID AAW17849 standard; protein; 752 AA.

XX

AC AAW17849;

XX

DT 27-AUG-2003 (revised)

DT 07-AUG-1997 (first entry)

XX

DE Hamster cytosolic phospholipase A2/B.

XX

Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

KW inflammation; inhibitor; antiinflammatory; CHO.

XX

Cricetus.

OS

XX

QY 607 TLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPVTCVDVFRPSNPWELAKT 666
DB |||||
661 TLDAMTEIHEYNQDLIRKQANKVKKLSIVSLGTGRSPQVPVTCVDVFRPSNPWELAKT 720
QY 667 VFGAKELGKQVVDCTDPDGR 687
DB |||||
721 VFGAKELGKQVVDCTDPDGR 741

RESULT 8
ABM84355
ID ABM84355 standard; protein; 810 AA.
AC
XX
XX
XX
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
XX N-PSDB; ACN43007.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 810 AA;

Query Match 98.3%; Score 3563; DB 8; Length 810;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 686; Conservative 0; Mismatches 1; Indels 58; Gaps 2;
QY 1 MQPFGRLVNTFSGVNTLFSNPRVKEVAVADVTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB |||||
1 MQPFGRLVNTFSGVNTLFSNPRVKEVAVADVTSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHLDLIRNHPWS 120
DB |||||
61 NPNRSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHLDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRII-----SCANCAENE 152
DB |||||
121 SVAHLAVELGIRECFHHSRIIIRVSAHQVPLGWLWELISTHTEIFSPKXSCANCAENE 180
QY 153 CTPHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVQLLGRNAVAG 212
DB |||||
181 CTPHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVQLLGRNAVAG 240
QY 213 LNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINMGNGYPIHSAMKFSQKGCAMII 272
DB |||||
241 LNQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINMGNGYPIHSAMKFSQKGCAMII 300
QY 273 SMDSSQIHSKDPYRGASPLHWAQNAEMARMLLKRCNCNVNSTSSAGNTALHVGVMRNFDC 332
DB |||||
301 SMDSSQIHSKDPYRGASPLHWAQNAEMARMLLKRCNCNVNSTSSAGNTALHVAVMRNFDC 360
QY 333 AIVLLTHGANADARGEHGNTPHLAMSKDNVEMIKALIVFGAEVDPNDPGETPTFLASK 392
DB |||||
361 AIVLLTHGANADARGEHGNTPHLAMSKDNVEMIKALIVFGAEVDPNDPGETPTFLASK 420
QY 393 IGRQLODLWHISRARKPAPILGSMRDEKRTDHLCLDGGGVKGLIIQLLTAIERKASGV 452
DB |||||
421 IGRQLODLWHISRARKPAPILGSMRDEKRTDHLCLDGGGVKGLIIQLLTAIERKASGV 480
QY 453 ATKDLFDWVAGTSTGGIILALAILHKSMAVMRGMFRMKDEVFRGSRPYESGLEEFLLKR 512
DB |||||
481 ATKDLFDWVAGTSTGGIILALAILHKSMAVMRGMFRMKDEVFRGSRPYESGLEEFLLKR 540
QY 513 EFGHEKMTDVRKPK-----VMLTGTLSDRQPAEL 542
DB |||||
541 EFGHEKMTDVRKPKLDQSDTPPALPERACFAGMVRGEAHLSTRTEYMLTGTLSDRQPAEL 600
QY 543 HLFRNYDAPETVREPRENVNLRPPAOPSDOLVWRAESSGAAPYFRPNGRFLDGLL 602
DB |||||
601 HLFRNYDAPETVREPRENVNLRPPAOPSDOLVWRAESSGAAPYFRPNGRFLDGLL 650
QY 603 ANNPILDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWE 662
DB |||||
661 ANNPILDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWE 720
QY 663 LAKTVFGAKELGKQVVDCTDPDGR 687
DB |||||
721 LAKTVFGAKELGKQVVDCTDPDGR 745

RESULT 9
ABM84354
ID ABM84354 standard; protein; 810 AA.
XX
XX ABM84354;
XX
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX

Db	181	VTDYKGETVFHYAVQDQNSQVQLLGRNAVAGLNVNNGQLTPLHLACQLGQKQWVRVLL	240
Qy	241	LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA	300
Db	241	LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA	300
Qy	301	RMLLRGCGNVNSTSAGNTALHVGWNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360
Db	301	RMLLRGCGNVNSTSAGNTALHVGWNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360
Qy	361	DNVEMIKALIVFGAEVDTNDGFTPLASKIGR-----QLQDLMHISRAKPAFILGSMRDEKTRTHDL	426
Db	361	DNVEMIKALIVFGAEVDTNDGFTPLASKIGRLVTRKAILTLRTVGAECYCPPIHG	420
Qy	396	-----QLQDLMHISRAKPAFILGSMRDEKTRTHDL	480
Db	421	VPAEQGSAAPHHPFSLERAQPPISLNLELQDLMHISRAKPAFILGSMRDEKTRTHDL	480
Qy	427	LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM	486
Db	481	LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM	540
Qy	487	YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDROPALHLFR	546
Db	541	YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDROPALHLFR	600
Qy	607	TLDAMTEIHEYNDQLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT	666
Db	661	TLDAMTEIHEYNDQLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPNPNWELAKT	720
Qy	667	VFGAKELGKVVDCCTDDPGR	687
Db	721	VFGAKELGKVVDCCTDDPGR	741
RESULT 7			
AD019776			
ID	AD019776	standard; protein; 806 AA.	
XX	AC	AD019776;	
XX	DT	12-AUG-2004 (first entry)	
XX	DE	Human PRO polypeptide #350.	
XX	KW	Human; PRO; immune related disorder; systemic lupus erythematosus;	
KW	KW	rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;	
KW	KW	systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;	
KW	KW	autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;	
KW	KW	diabetes mellitus; renal disease; demyelinating disease;	
KW	KW	central nervous system; peripheral nervous system;	
KW	KW	demyelinating polyneuropathy; Guillain-Barre syndrome;	
KW	KW	chronic inflammatory demyelinating polyneuropathy.	
XX	OS	Homo sapiens.	
XX	PN	WO2004043361-A2.	
XX	PD	27-MAY-2004.	
XX	PD	06-NOV-2003; 2003WO-US035268.	
XX	PR	08-NOV-2002; 2002US-0425235P.	
XX	PA	(GETH) GENENTECH INC.	
XX	PI	Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;	
PI	PI	Wood WI, Wu TD;	

XX	WPI; 2004-420067/39.		
DR	N-PSDB; AD019775.		
XX	Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for		
PT	treating an immune related disorder such as systemic lupus erythematosus,		
PT	rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or		
PT	spondyloarthropathy.		
XX	Claim 7; SEQ ID NO 700; 1731pp; English.		
XX	The invention relates to human PRO polypeptides and the polynucleotides		
CC	encoding them. The polypeptides and polynucleotides are useful for		
CC	treating and diagnosing immune related disorders in mammals. The immune		
CC	related disorders include systemic lupus erythematosus, rheumatoid		
CC	arthritis, osteoarthritis, juvenile chronic arthritis, systemic		
CC	sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune		
CC	haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes		
CC	mellitus, immune-mediated renal disease, demyelinating diseases of the		
CC	central or peripheral nervous system, demyelinating polyneuropathy,		
CC	Guillain-Barre syndrome and chronic inflammatory demyelinating		
CC	polyneuropathy. This sequence represents a human PRO polypeptide of the		
XX	invention.		
XX	Sequence 806 AA;		
Qy	Query Match	98.5%; Score 3572; DB 8; Length 806;	
Db	Best Local Similarity	92.4%; Pred. No. 0;	
Qy	Matches	685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;	
Qy	1	MOFFRLVNTSGVNTLFSNPRVKEVAVADVTSSDRVREEQQLILFQNTNRTWDCVILV	60
Db	1	MOFFRLVNTSGVNTLFSNPRVKEVAVADVTSSDRVREEQQLILFQNTNRTWDCVILV	60
Qy	61	NPRNSQSGFRLEADALVNFHOYSQSLPPFYESSQVLTHTVQLHTLIRNHPSW	120
Db	61	NPRNSQSGFRLEADALVNFHOYSQSLPPFYESSQVLTHTVQLHTLIRNHPSW	120
Qy	121	SVLAHVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD	180
Db	121	SVLAHVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD	180
Qy	181	VTDYKGETVFHYAVQDQNSQVQLLGRNAVAGLNVNNGQLTPLHLACQLGQKQWVRVLL	240
Db	181	VTDYKGETVFHYAVQDQNSQVQLLGRNAVAGLNVNNGQLTPLHLACQLGQKQWVRVLL	240
Qy	241	LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA	300
Db	241	LCNARCNIIMPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA	300
Qy	301	RMLLRGCGNVNSTSAGNTALHVGWNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360
Db	301	RMLLRGCGNVNSTSAGNTALHVGWNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360
Qy	361	DNVEMIKALIVFGAEVDTNDGFTPLASKIGR-----	395
Db	361	DNVEMIKALIVFGAEVDTNDGFTPLASKIGRLVTRKAILTLRTVGAECYCPPIHG	420
Qy	396	-----QLQDLMHISRAKPAFILGSMRDEKTRTHDL	426
Db	421	VPAEQGSAAPHHPFSLERAQPPISLNLELQDLMHISRAKPAFILGSMRDEKTRTHDL	480
Qy	427	LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM	486
Db	481	LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM	540
Qy	487	YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDROPALHLFR	546
Db	541	YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDROPALHLFR	600
Qy	547	NYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNRFLDGLLANNP	606
Db	601	NYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNRFLDGLLANNP	660

PT Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PS phospholipase activity, is active in the absence of calcium.
PS Claim 6; Page 23-25; 41pp; English.
XX
CC The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
XX 19a)
XX
SQ Sequence 687 AA;
Query Match 99.5%; Score 3606.5; DB 5; Length 687;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTFGVTLNFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFGVTLNFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFQLELEADALNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPNRSQSGRLFQLELEADALNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVRNRPDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
DB 301 RMLLKRCGNVNTSSAGNTALHVGVRNRPDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
QY 361 DNVEIMKALIVGAEDVTNDPGETPTFLASKIGROLQDLMHISRARKPAFILGSMRDEK 420
DB 361 DNVEIMKALIVGAEDVTNDPGETPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
QY 421 RTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGILAILHLSKSM 480
DB 420 RTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGILAILHLSKSM 479
QY 481 AYMRGMYFMKDEVFGRSPYEGSGLPEEFLKRFEGEHTKMTDVRKPKVMTGTLSRQPA 540
DB 480 AYMRGMYFMKDEVFGRSPYEGSGLPEEFLKRFEGEHTKMTDVRKPKVMTGTLSRQPA 539
QY 541 ELHLFRNYDAPETVREPRNQNLPRPAQPSDQLVRAARSSGAAPTFRPNRGFLDGG 600
DB 540 ELHLFRNYDAPETVREPRNQNLPRPAQPSDQLVRAARSSGAAPTFRPNRGFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNQDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNQDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659

DB 600 LLANNPTLDAMTEIHEYNQDLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688
DB 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
RESULT 6
AAE25968
ID AAE25968 standard; protein; 806 AA.
XX AAE25968;
AC AAE25968;
XX 15-NOV-2002 (first entry)
DT Human PLA2 group VI (Ca2+-independent) protein.
XX
DE Human; antisense; phospholipase A2; infection; inflammation; tumour;
XX antisense therapy; PLA2 protein.
KW
XX Homo sapiens.
OS
XX US6410325-B1.
PN
XX 25-JUN-2002.
PD
XX 09-MAY-2001; 2001US-00851896.
PF
XX 09-MAY-2001; 2001US-00851896.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Bennett CF, Freier SM, Watt AT;
PI
XX WPI; 2002-616513/66.
DR
XX N-PSDB; AAD42941.
PT Novel antisense compounds useful for inhibiting gene expression of human
PT phospholipase A2, group VI and for treating diseases associated with
PT expression of phospholipase A2, group VI.
XX
PS Disclosure; Col 109-116; 72pp; English.
XX
CC The present invention relates to novel antisense compounds which inhibit
CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
CC The invention is useful for inhibiting the expression of PLA2, group VI
CC (Ca2+-independent) in human cells or tissues and for treating an animal,
CC particularly a human suspected of having or being prone to a disease or
CC condition associated with expression of human PLA2, group VI (Ca2+-
CC independent). It is useful for diagnostics, therapeutics and as research
CC reagent, e.g. prophylactically to prevent or delay infection, tumour
CC formation or inflammation. The present sequence is human PLA2 group VI
CC (Ca2+-independent) protein
XX
SQ Sequence 806 AA;
Query Match 98.5%; Score 3572; DB 5; Length 806;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;
QY 1 MQFFGRLVNTFGVTLNFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFGVTLNFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFQLELEADALNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPNRSQSGRLFQLELEADALNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGELLVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240

QY 661 WELAKTVFGAKELGKRWVDDCCTDPDGR 687
 DB 693 WELAKTVFGAKELGKRWVDDCCTDPDGR 719

RESULT 4

AAW17847
 ID AAW17847 standard; protein; 687 AA.

AC AAW17847;

DT 07-AUG-1997 (first entry)

DE Cytosolic phospholipase A2/B (alternatively spliced clone 19a).

KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 inflammation; inhibitor; antiinflammatory.

OS Homo sapiens.

PN WO9717448-A2.

PD 15-MAY-1997.

PF 07-NOV-1996; 96WO-US017794.

PR 08-NOV-1995; 95US-00555568.

XX (GENY) GENETICS INST INC.

PI Jones S, Tang J;

DR WPI; 1997-281037/25.

DR N-PSDB; AAT68825.

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a

PT mammalian subject.

PS Claim 12; Page 49-51; 74pp; English.

XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
 CC characterised by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839- 44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17845)
 CC and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes
 CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade

XX Sequence 687 AA;

Query Match 99.5%; Score 3606.5; DB 2; Length 687;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

DB 1 MQFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLQLELEADALVNFHOYSQQLIPFYESSQVLTHTVLOHLTDLIRNHPSW 120

DB 61 NPNRSQSGRLQLELEADALVNFHOYSQQLIPFYESSQVLTHTVLOHLTDLIRNHPSW 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGELLVELVQYCHTQMD 180

DB 121 SVAHLAVALGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGELLVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTFLHLACQLGKQEMVRVLL 240

DB 181 VTDYKGETVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTFLHLACQLGKQEMVRVLL 240
 QY 241 LCNARCNIMGNGYPPIHSAMKFSQKCAEMIISMDSSQIHSDPKRYGASPLHWAQNAEWA 300
 DB 241 LCNARCNIMGNGYPPIHSAMKFSQKCAEMIISMDSSQIHSDPKRYGASPLHWAQNAEWA 300
 QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDPNDPGETPTFLASKIGRQLODLMIHSRARKPAFTLGSMRDEK 420
 DB 361 DNVEMIKALIVFGAEVDPNDPGETPTFLASKIGR- LQDLMIHSRARKPAFTLGSMRDEK 419
 QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 480
 DB 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSXM 479
 QY 481 AYMRGMYFRMKDEVPRGSRPYESGPLEFLKREFGHEHTMTDVRKPKVMLTGTLSDRQPA 540
 DB 480 AYMRGMYFRMKDEVPRGSRPYESGPLEFLKREFGHEHTMTDVRKPKVMLTGTLSDRQPA 539
 QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRNGRFLDGG 600
 DB 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRNGRFLDGG 599
 QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSPNP 660
 DB 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSPNP 659
 QY 661 WELAKTVFGAKELGKRWVDDCCTDPDGR 687
 DB 660 WELAKTVFGAKELGKRWVDDCCTDPDGR 687

RESULT 5

ABB82231
 ID ABB82231 standard; protein; 687 AA.

AC ABB82231;

DT 08-JAN-2003 (first entry)

XX Human cPLA2/B splice variant (clone 19a).

DE Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
 KW antiasthmatic; human.

OS Homo sapiens.

PN US2002106364-A1.

PD 08-AUG-2002.

XX 09-AUG-2001; 2001US-00927180.

XX 27-JUL-1994; 94US-00281193.

PR 14-APR-1995; 95US-00422106.

PR 14-APR-1995; 95US-00422420.

PR 26-JUN-1995; 95WO-US008069.

PR 08-NOV-1995; 95US-00555568.

PR 09-SEP-1998; 98US-00149988.

PR 06-MAR-2000; 2000US-00519223.

XX (GENY) GENETICS INST INC.

XX Jones S, Tang J;

XX WPI; 2002-739923/80.

DR N-PSDB; ABV73010.

Db 301 RMLLRKGCNNVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK 420
Db 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK 420
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFOWVAGTSTGGILALAILHSKSM 480
Db 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFOWVAGTSTGGILALAILHSKSM 480
QY 481 AYMRGMYFMKDEVFGRSPYSGPLEEFLKRFGHEHTKMDVRKPKVMTGTLSDRQPA 540
Db 481 AYMRGMYFMKDEVFGRSPYSGPLEEFLKRFGHEHTKMDVRKPKVMTGTLSDRQPA 540
QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPDLVRAARSSGAAPTFRPNRGLDGG 600
Db 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPDLVRAARSSGAAPTFRPNRGLDGG 600
QY 601 LLANNPTLDAMTEIHEYNDLIRKGQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
Db 601 LLANNPTLDAMTEIHEYNDLIRKGQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 3
ADD93407
ID ADD93407 standard; protein; 784 AA.
AC ADD93407;
XX
DT 29-JAN-2004 (first entry)
DE Human lipid-associated molecule LIPAM-14 polypeptide.
XX
KW Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
KW antichryoid; antidiabetic; cytostatic; dermatological; immunosuppressive;
KW antiinflammatory; thymometric; antiallergic; cerebroprotective;
KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;
KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
KW virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
KW nootropic.
XX
OS Homo sapiens.
XX
PN WO2003083081-A2.
XX
PD 09-OCT-2003.
XX
PF 27-MAR-2003; 2003WO-US009755.
XX
PR 29-MAR-2002; 2002US-0368722P.
PR 03-MAY-2002; 2002US-0377576P.
PR 05-JUL-2002; 2002US-0393914P.
PR 27-SEP-2002; 2002US-0414269P.
XX
PA (INCY-) INCYTE CORP.
PI Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;
PI Baughn MR, Lee EA, Griffin JA, Kahle AE, Elliott VS, Chang H;
PI Lee S, Ramkumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;
PI Jackson AA;
XX
DR WPI; 2003-788347/74.
DR N-PSDB; ADD93426.
XX
PT New LIPAM polypeptides, useful for diagnosing, preventing, and treating
PT disorders associated with abnormal expression or activity of LIPAM, e.g.
PT neuromuscular, immunological, cardiovascular disorders, cancer and/or
PT infections.
XX

PS XX
Claim 69; Page 206-207; 238pp; English.
The present sequence is the protein sequence of human lipid-associated molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows homology to human Ca²⁺-independent phospholipase A2 short isoform. This is one of 19 LIPAM polypeptides of the invention. The invention relates to these novel LIPAMs and the nucleic acids encoding them, and to the use of nucleic acids and proteins in the diagnosis, treatment and prevention of disorders associated with abnormal expression or activity of LIPAM such as neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy, catatonial), endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g. leukemia, cervical or breast cancers), immunological disorders (e.g. scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention also relates to the assessment of the effects of exogenous compounds on the expression of nucleic acids and LIPAMs. The invention provides expression vectors, host cells, antibodies, agonists and antagonists, transgenic organisms, and arrays and microarrays of the polynucleotides.
XX
SQ Sequence 784 AA;
Query Match 99.6%; Score 3612; DB 7; Length 784;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 686; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFGVNTLFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 33 MQFFGRLVNTFGVNTLFSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 92
QY 61 NPRNSQSGRLFLQLELEADALVNFHQYSQQLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
Db 93 NPRNSQSGRLFLQLELEADALVNFHQYSQQLPFYESSQVLTHTVQLHQLTDLIRNHPW 152
QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDGRIILVELVOYCHTOMD 180
Db 153 SVAHLAVALGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDGRIILVELVOYCHTOMD 212
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 213 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 272
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPHYGASPLHWAKNAEMA 300
Db 273 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPHYGASPLHWAKNAEMA 332
QY 301 RMLLRKGCNNVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 333 RMLLRKGCNNVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 392
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK 420
Db 393 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIGRQLQDLMLHISRARKPAFILGSMRDEK 452
QY 421 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFOWVAGTSTGGILALAILHSKSM 480
Db 453 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFOWVAGTSTGGILALAILHSKSM 512
QY 481 AYMRGMYFMKDEVFGRSPYSGPLEEFLKRFGHEHTKMDVRKPKVMTGTLSDRQPA 540
Db 513 AYMRGMYFMKDEVFGRSPYSGPLEEFLKRFGHEHTKMDVRKPKVMTGTLSDRQPA 572
QY 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPDLVRAARSSGAAPTFRPNRGLDGG 600
Db 573 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPSPDLVRAARSSGAAPTFRPNRGLDGG 632
QY 601 LLANNPTLDAMTEIHEYNDLIRKGQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
Db 633 LLANNPTLDAMTEIHEYNDLIRKGQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 692

XX	SQ	Sequence 688 AA;	
		Query Match	100.0%; Score 3625; DB 2; Length 688;
		Best Local Similarity	100.0%; Pred. No. 0;
		Matches 688; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60
DB	1	MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60
QY	61	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW	120
DB	61	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW	120
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIIVELVQYCHTQMD	180
DB	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIIVELVQYCHTQMD	180
QY	181	VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGQKQEMVRVLL	240
DB	181	VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGQKQEMVRVLL	240
QY	241	LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYKASPLHWAKNAENA	300
DB	241	LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYKASPLHWAKNAENA	300
QY	301	RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360
DB	301	RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360
QY	361	DNVEMIKALIVFGAEVDTNPDEGTFPLASKIGRQQLQDLMIHSRARKPAFTILGSMRDEK	420
DB	361	DNVEMIKALIVFGAEVDTNPDEGTFPLASKIGRQQLQDLMIHSRARKPAFTILGSMRDEK	420
QY	421	RTDHLCLLDGGVGLIIIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHKSXM	480
DB	421	RTDHLCLLDGGVGLIIIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHKSXM	480
QY	481	AYMRGMYFRMKDEVFRGSPYSGPLEEFLKEFGEHTQWTVRKPKNMLTGTLSDRQPA	540
DB	481	AYMRGMYFRMKDEVFRGSPYSGPLEEFLKEFGEHTQWTVRKPKNMLTGTLSDRQPA	540
QY	541	ELHLFRNYDAPETVREPQNQVNRPPAQPQSDQLVWRAARSGAAPTFRPNRFLDGG	600
DB	541	ELHLFRNYDAPETVREPQNQVNRPPAQPQSDQLVWRAARSGAAPTFRPNRFLDGG	600
QY	601	LIANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCYDVFPRSPNP	660
DB	601	LIANNPTLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPVTCYDVFPRSPNP	660
QY	661	WELAKTVFGAKELGKMWVDCCTDPDGRP	688
DB	661	WELAKTVFGAKELGKMWVDCCTDPDGRP	688
RESULT 2			
ID	ABB82232		
XX	ABB82232	standard; protein; 688 AA.	
AC	ABB82232;		
XX	ABB82232;		
DT	08-JAN-2003	(first entry)	
DE	Human cPLA2/B splice variant (clone 19b).		
XX	Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;		
KW	antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;		
XX	antiasthmatic; human.		
OS	Homo sapiens.		
XX	US2002106364-A1.		
PN			

XX	PD	08-AUG-2002.	
XX	PF	09-AUG-2001; 2001US-00927180.	
XX	PR	27-JUL-1994; 94US-00281193.	
XX	PR	14-APR-1995; 95US-00422106.	
XX	PR	14-APR-1995; 95US-00422420.	
XX	PR	26-JUN-1995; 95WO-US008069.	
XX	PR	08-NOV-1995; 95US-00555568.	
XX	PR	09-SEP-1998; 98US-00149988.	
XX	PR	06-MAR-2000; 2000US-00519223.	
XX	PA	(GEMY) GENETICS INST INC.	
XX	PI	Jones S, Tang J;	
XX	XX	WPI: 2002-739923/80.	
DR	DR	N-PSDB; ABV73011.	
XX	XX	Novel composition comprising purified mammalian calcium independent	
PT	PT	phospholipase enzyme, useful for the screening of inhibitors of	
PT	PT	phospholipase activity, is active in the absence of calcium.	
XX	XX	Claim 6; Page 28-30; 41pp; English.	
XX	XX	The invention relates to a purified mammalian calcium independent	
CC	CC	cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is	
CC	CC	characterized by activity in the absence of calcium and has a molecular	
CC	CC	weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified	
CC	CC	calcium independent phospholipase enzyme is useful for identifying an	
CC	CC	inhibitor of phospholipase activity which involves combining (I),	
CC	CC	phospholipid and candidate inhibitor compound, and observing whether the	
CC	CC	enzyme cleaves the phospholipid and releases fatty acid from it. A	
CC	CC	pharmaceutical composition (PC) comprising a therapeutically effective	
CC	CC	amount of the inhibitor is useful for reducing inflammation and for	
CC	CC	treating inflammatory conditions including rheumatoid arthritis,	
CC	CC	psoriasis, asthma, inflammatory bowel disease and other diseases mediated	
CC	CC	by increased levels of prostaglandins, leukotriene or platelet activating	
CC	CC	factor. A composition comprising an antibody which binds to (I) is useful	
CC	CC	as research and diagnostic tool, and is also useful in the study of	
CC	CC	phospholipase A2 activity and inflammatory conditions. The present	
CC	CC	sequence represents a human cPLA2/B enzyme longer splice variant (clone	
CC	CC	19b)	
XX	SQ	Sequence 688 AA;	
		Query Match	100.0%; Score 3625; DB 5; Length 688;
		Best Local Similarity	100.0%; Pred. No. 0;
		Matches 688; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60
DB	1	MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60
QY	61	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW	120
DB	61	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW	120
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIIVELVQYCHTQMD	180
DB	121	SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEIIVELVQYCHTQMD	180
QY	181	VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGQKQEMVRVLL	240
DB	181	VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGQKQEMVRVLL	240
QY	241	LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYKASPLHWAKNAENA	300
DB	241	LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYKASPLHWAKNAENA	300
QY	301	RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK	360

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 88.7957 Seconds
(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFFGLVNTFGVTNLFNS.....GAKELGKMVVDCCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3625	100.0	688	2	AAW17848	Cytosolic
2	3625	100.0	688	5	ABB82232	Human cpl
3	3612	99.6	784	7	ADP93407	Human lip
4	3606.5	99.5	687	2	AAW17847	Cytosolic
5	3606.5	99.5	687	5	ABB82231	Human cpl
6	3572	98.5	806	5	Aae25968	Human PLA
7	3572	98.5	806	8	ADO19776	Human PRO
8	3563	98.3	810	8	ABM84355	Human dia
9	3563	98.3	810	8	ABM84354	Human dia
10	3315	91.4	752	2	AAR83018	Calcium-i
11	3315	91.4	752	2	AAW01479	Calcium-i
12	3315	91.4	752	2	AAW13163	Ca-indepe
13	3315	91.4	752	2	AAW17849	Hamster c
14	3315	91.4	752	2	AAW81825	Chinese h
15	3315	91.4	752	5	ABB82215	Calcium i
16	3269.5	90.2	751	7	AD046244	Rat Prote
17	3269.5	90.2	751	7	AD560532	Rat Prote
18	3269.5	90.2	751	7	AD552230	Rat Prote
19	3269.5	90.2	751	7	AD560536	Rat Prote
20	2728.5	75.3	667	7	ADM05093	Human pro
21	2084	57.5	394	2	AAW17845	Cytosolic
22	2084	57.5	394	5	ABB82229	Calcium i
23	1696	46.8	401	4	AAW92811	Human pro
24	1531	42.2	292	2	AAW17846	Cytosolic
25	1531	42.2	292	5	ABB82230	Calcium i

RESULT 1

AAW17848
ID AAW17848 standard; protein; 688 AA.

XX AC AAW17848;

XX DT 07-AUG-1997 (first entry)

XX DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).

XX KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory.

XX OS Homo sapiens.

XX PN WO9717448-A2.

XX PD 15-MAY-1997.

XX PF 07-NOV-1996; 96WO-US017794.

XX PR 08-NOV-1995; 95US-00555568.

XX (GEMY) GENETICS INST INC.

XX Jones S, Tang J;

XX WPI; 1997-281037/25.

XX N-PSDB; AAT68826.

XX Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

XX Claim 12; Page 54-56; 74pp; English.

XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl phosphate and by a lack of stimulation by ATP, by a pH optimum of 6, a lack of the amino acid sequences given in AAW17839- 44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

ALIGNMENTS

AC	Q810Q6;	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Hypothetical protein W07A8.2b.	
GN	Name=W07A8.2b; ORFNames=W07A8.2;	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Peloderinae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=Bristol N2;	
RC	MEDLINE=99069613; PubMed=9851916;	
RX	none;	
RA	"Genome sequence of the nematode C.elegans: A platform for	
RT	investigating biology.";	
RL	Science 282:2012-2018(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Bristol N2;	
RA	Basham V.M.;	
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Bristol N2;	
RA	Ainscough R.;	
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AL021489; CAD54162.1; JOINED.	
DR	EMBL; Z82075; CAD54162.1; -.	
DR	EMBL; AL021489; CAD54166.1; -.	
DR	EMBL; Z82075; CAD54166.1; JOINED.	
DR	HSSP; Q60778; 10Y3.	
DR	WormBase; WBGene00012319; W07A8.2.	
DR	WormPep; W07A8.2b; CE32002.	
DR	GO; GO:0003824; F:catalytic activity; IEA.	
DR	GO; GO:0045735; F:nutrient reservoir activity; IEA.	
DR	InterPro; IPR002110; ANK.	
DR	InterPro; IPR002641; Patatin.	
DR	Pfam; PF01734; Patatin; 1.	
DR	PRINTS; PR01415; ANKYRIN.	
DR	SMART; SMO0248; ANK; 7.	
DR	PROSITE; PSS0088; ANK REPEAT; 2.	
DR	PROSITE; PS0297; ANK REP REGION; 1.	
KW	ANK repeat; Hypothetical protein.	
SQL	SEQUENCE 1021 AA; 114268 MW; 22E77A0FAF015E37 CRC64;	
Query Match 17.2%; Score 622; DB 2; Length 1021;		
Best Local Similarity 23.9%; Pred. No. 2.4e-38;		
Matches 184; Conservative 153; Mismatches 284; Indels 150; Gaps 23;		
QY	39 REEQQLILFQNTPRNTWDCVLVPRNSQSGFRLQLEAD--ALVNFHQYSSQLLPYE 96	
DB	204 KEEEL---KNKPLYHLAIIYNNENKYMVLSFRSHKLDVVALCERCENPELFRVFP 260	
QY	97 SSPQV---LHTEVLQHLTDLRNHPSPVAHLAVELGIRECFHH---SRIISCANCAENE 150	
DB	261 KNNVNIKDYLT-----IFPELRDNNWTKSVHISKIGLLEFENKKEHLKYNLIVQP 315	
QY	151 EGCPTPLHACKRGDGEILVELVQYCHTQOMVTDYKGETVFHYAVQGDNSQVLQLL--GRN 208	
DB	316 EGLSPMLIAVQNTQIETVSMWLDH-GADINILSSEGQNVLHVAATASSGDLIKILWETKK 374	
QY	209 AVAGLNQNNQGLTFLHLACQGHQEMVRVLLLCNARCNMGPNG-----YPI 256	
DB	375 CETMINQNTDSNGYTPAYVA-----LINACLNSCQTLRGFGGIGQSSDSTQMANPI 424	
QY	257 HSAKMFQ--KGCAEMIISDSSOIHSDKPRYGASPLHWKNAEMRMLLKR---GCNVN 311	
DB	425 IGAMRGKLDVSLRKMLLEKQDGTEPTTGTNTVTHCAINKKCLILLMEKFRDQTDPE 484	
QY	312 STSAGNTALHVGVRNRFDCAI VLLTHGANADARGEHNTPLHLAMSKNVEMIKALIV 371	


```
Db 563 LLCLDGGGIRGLVLMLEIEKLSRTPPIHMFDMWTAGTGTGGILALALGCGTKWRQMG 622
QY 486 MYFRMKDVEFRGSRPYSGPLBEFLKRGEGHTKMTDVKRKPVMLTGTLSDRQPAELHLF 545
Db 623 LYLRMKEQCFVGSRPYNSEFFESILKDNIGFNVMTDIKHPKIMVTGVNADRPVDLHLF 682
QY 546 RNYDAPETVR---EPFNQVNLRPAPQSDOLVWRAABSSGAAPYFRPNRGFLDGGLL 602
Db 683 RNYTSASDILGIVTPINNRI---PPQPSQLVWRAARATGAAPSYFRAFGRFLDGGLL 739
QY 603 ANNPITLDAMTEIHEYNQDLIRKQANKVKKLSVSLGTGRSPQVPVTCVDFVRPSNPWE 662
Db 740 ANNPITLDAMTEIHEYNMALSAGRESAIPVSVMSLGTGHIPTVELKDIDVFRPESIW 799
QY 663 LAKTVFGAKELGKVVDCCTDDPGR 687
Db 800 TAKLAYGISTIGNLLVDQATCSDGR 824

RESULT 12
Q8MR13 PRELIMINARY; PRT; 386 AA.
AC Q8MR13;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE LD44515p.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fribe E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY121212; AAMS2704.1; -.
DR FlyBase; FBgn0036053; CG6718.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 386 AA; 42693 MW; B32B7BCFC38541DD CRC64;

Query Match 20.5%; Score 741.5; DB 2; Length 386;
Best Local Similarity 43.1%; Pred. No. 4.3e-48;
Matches 155; Conservative 55; Mismatches 109; Indels 41; Gaps 4;

QY 331 DCAIVLLTGANADARGEHTPLHMSKONVEMIKALIVGAEDVTPNDGTFPTFLA 390
Db 2 DALLGFTTKVNAD-----EMKKNSSDLSAGSKSAVSSPEQLPSPSTPIA 49
QY 391 SKTIGROLQDLMLHSRARKPAFILGSMRDEKRTDHLCLDGGVKGGLIIILIAIEKAS 450
Db 50 AETG-----DKPYGRGLLCLDGGGIRGLVLMLEIEKLS 86
QY 451 GVATKDLFDWAGTSTGGILALAILHSGMAYVRGMVFRMKDVEFRGSRPYSGPLEEPL 510
Db 87 RTPPIHMFDMWTAGTSTGGILALALGCGTKWRQMGILYLRMKEQCFVGSRPYNSEFFESIL 146
QY 511 KREFGHHTKMTDVKRKPVMLTGTLSDRQPAELHLFRNYDAPETVR---EPFNQVNLRP 567
Db 147 KNLGFEFNVTDIKHPKIMVTGVNADRPVDLHLFRNYTSASDILGIVTPINNRI---P 203
QY 568 PAQPSDOLVWRAABSSGAAPYFRPNRGFLDGGILANNPTLDAMTEIHEYNQDLIRKQOA 627
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Db 204 PPQPSQLVWRAARATGAAPSYFRAFGRFLDGGILANNPTLDAMTEIHEYNMALSAGRE 263
QY 628 NKVKKLSIVSLGTGRSPQVPVTCVDFVRPSNPWELAKTVFGAKELGKVVDCCTDDPGR 687
Db 264 SEAIIPSVMSLGTGHIPTVELKDIDVFRPESIWDTAKLAYGISTIGNLLVDQATCSDGR 323

RESULT 13
Q20500 PRELIMINARY; PRT; 1071 AA.
AC Q20500;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE Hypothetical protein F47A4.5.
GN ORFNames=F47A4.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RL investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Mortimore B.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z49888; CAA90061.1; -.
DR PIR; T22327; T22327.
DR WormBase; WBGene00009801; F47A4.5.
DR WormPep; F47A4.5; C802248.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR InterPro; IPR001638; SBP bac_3.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00023; Ank; 5.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK REPEAT; 3.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS01039; SBP_BACTERIAL_3; UNKNOWN_1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 1071 AA; 119089 MW; 138067CA3E31C1D5 CRC64;

Query Match 18.0%; Score 651; DB 2; Length 1071;
Best Local Similarity 27.1%; Pred. No. 1.5e-40;
Matches 195; Conservative 125; Mismatches 260; Indels 140; Gaps 20;

QY 69 FRLFLELEADALVNFHVOYSSQLLPFYESSQVQLHTEVL---OHLTDLIRNHPSVVAH 124
Db 315 FSLFRATDKKLDMLLHLCDKEKSLFTSLDSTMTRADIIRSKIEELVQIRLKPYYMH 374
QY 125 LAVELGIRECFHHSRI-----ISCANCAENEECTPLHLACRKGDSILVELVOY 174
Db 375 VAIAITDRLDFFSDGMIKTMNETLEPFESQLRCLCHTENCYPVHLALTMDROKI VERLLEL 434
QY 175 CHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG---LNQVNNQGLTPLHLACQLG 231
Db 435 DPTLFCETDKAGNVMHVH---NSSFCAQIIWDRCPASQHFIDERNMDGQSPLEAVSTA 491
QY 232 KQEMVRVLLLCNARCINMGPNGYPIHSAKFSOKGCAEMIISM-----DSS 277
Db 492 KPLVATFL-----LGKAKFTRGDRNELFVAMTSKNAQSVVEVVLTDKP 535
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QY 121 SVAHLAVELGIRECPHSHSIIISCANCAENEBGCTPLHLACRKGDEGILLVELVVOYCHTQMD 180
Db 121 SLAHVAVEIGLSEFKHGLISLNSTCEDGCTPLHLACKKGIDNCLQELVEECQARLD 180
QY 181 VTDYKGETVFHYAVQDQNSQVQLLGRNAVAGLNOVNOGLTPLHLACOLGQOEMVRVLL 240
Db 181 IADQNGETVYHAAQONNPRVIEILCSVPSGVNKHNNNETPLHVACHLGTGLVLALL 240
QY 241 LCNARCNTMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 RCHARDIIGKDGYPHTAMKYSQKECVBAILDVSASQLHABDPRYQATPIHWAKNAEMA 300
QY 301 RMLLKGCCNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RLIIERGCVNSTSKTDLPLHIMWKDRFEAMVLLTNVADPNVKGHEHGNTPHLAMCK 360
QY 361 DNVEIMKALIVFGAEVDPNDGCTPTFLASIKIGLOQLMHISRAK-----PAFTLGSM 416
Db 361 DQLELIKALMWFGADVQEHNDGCTPTFLASIKIGLOQLMHISRAK-----PAFTLGSM 420
QY 417 REKRTDHLCLDGGGVKGLIIQLLIAEKASGVATKDLFDWVAGTSGTGILALAILH 476
Db 421 EDGLRVKDRLLCLDGGGIRGLVMQLLIAEKASGRPIRELFDMVSGTSGTGILALAIH 480
QY 477 SKSMAYMRGMYFRMKDEVERGSRPYESGPLEBFLKEEFGHTKMTDVRKPKVMTGLTSD 536
Db 481 GMPMSVRCLYFRMKNEVPHGRSPYESGPLEBFLKEEFGHTKMTDVRKPKVMTGLTSD 540
QY 537 ROPAEHLHFRNYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTYFRPNGRF 596
Db 541 RHPAEHLHFRNYDPPETDHEPPYKSVASFRPVTTPAEQLVWRAARSSGAAPTYFRPNGRF 600
QY 597 LDGGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIVSLGTRSPQVPTCVDPVR 656
Db 601 LDGGLLNNPTLDAMTEIHEYNTCLKKGMAGQVKGLGIWISLGTGKPPQISVSGVDVFR 660
QY 657 PSNPVELATVFGAKELGKQWVDCCTDPDG 686
Db 661 PSNPVEWMTVVGARELQKQWVDCCTDSDG 690

RESULT 8
Q6NWY0
ID Q6NWY0 PRELIMINARY; PRT; 818 AA.
AC Q6NWY0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE ZGC:77476.
GN ORFNames=ZGC:77476;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Hopkins R.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina M., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067375; AAH67375.1; -.
DR HSSP; P20749; 1K1B.
DR ZFIN; ZDB-GENE-040426-2079; zgc:77476.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 54.5%; Score 1974; DB 2; Length 818;
Best Local Similarity 50.5%; Pred. No. 7, 7e-142;
Matches 380; Conservative 122; Mismatches 183; Indels 68; Gaps 4;

QY 1 MQPFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVREBQQLILFQNTNRTWDCVLV 60
Db 1 MQPFLGRILDTSSVSSLSFNPRVDRVQLSDYNGKILHQEGRLALYRNQSQSDCLLL 60
QY 61 NPNRSQSGFRLEFQLEADALVNPFOYSSQLLPFYESSQVLTHTVLOHLTLIRNHPW 120
Db 61 CPESPSVALRFPQVASEEDAMNFFQYALKRPFTEMRLRPPKPEMLQIVDCVRNHPW 120
QY 121 SVAHLAVELGIRECPHSHSIIISCANCAENEBGCTPLHLACRKGDEGILLVELVVOYCHTQMD 180
Db 121 SSAHIAVDTGLRDLCKHNVILSQMN-SRDAQQTPLHLACERGDVGVCRELEECQARTD 179
QY 181 VTDYKGETVFHYAVQDQNSQVQLLGRNAVAGLNOVNOGLTPLHLACOLGQOEMVRVLL 240
Db 180 VKDKNGETPMHCAAKQDSALIIIEVLCAQACAGVNSLNAAGETPMHIAACRLGREVVVKGLL 239
QY 241 LCNARCNTMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 240 AGGARCDIWMNGGFFIHTAMKFSEKSCABAILSSPNQLLAEDPVYGGTPLHWAKTAMS 299
QY 301 RMLLKGCCNVNSTSAGNTALHVGVMNRFPDCAIVLLTHGANADARGEHGNTPHLAMSK 360
Db 300 RLLLDGRCNVNYSKGTGSPHLITKRGFRFEAAVMTLLTHGADANIRGQDGNALHLAMKL 359
QY 361 DNVEIMKALIVFGAEVDPNDGCTPTFLASKI----- 393
Db 360 DNMDLIKALMWFGADVQEHNDGCTPTFLIAAATSKGNSRKNVLLNMLCSVGERCHPPSLN 419
QY 394 -----GRQLQDLMHIS-----RARKPAFALIGSMRDEKRTDHLCLDGGGVKGLI 438
Db 420 SPTHSLRKAPPGIGDIDIMQVAVATVMSRGFVADGLKTKGNKMDRLCLDGGGKGLV 479
QY 439 ITQLLIAIEKASGVATKDLFDWVAGTSGTGILALIAILHSKSMAYMRGMYFRMKDEVFRGS 498
Db 480 LIQLLIAIEKASGRPIRELFDMVSGTSGTGILALIAIVHGSWEYLRLCYFRMKDEVFKGS 539
QY 499 RPYESGPLEEFLKREFGHTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPR 558
Db 540 RPYESGPLEEFLKNEFGHTKMTDVTTPRVVMTSVLADRHHPGELHLFRNYDPPALQDRPP 599
QY 559 FNQNVNLPAPQ-----SDQLVWRAARSSGAAPTYFRPN 593
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DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS0088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 807 AA; 89555 MW; 1B9018AE1B2D252F CRC64;

Query Match 90.1%; Score 3267.5; DB 2; Length 807;
Best Local Similarity 83.6%; Pred. No. 9.9e-241;
Matches 620; Conservative 31; Mismatches 36; Indels 55; Gaps 1;

QY 1 MOFFGRLVNTFSQVTLNFSNPRFKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSQVTLNFSNPRFKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLEADALVNFHFOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120
DB 61 SPNPSQSGRLFOLEADALVNFHFOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPW 120

QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFPHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVQYCHTQMD 180

QY 181 VTDYKETVFHYAQVDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDNKGETAFHYAQVDNSQVQLLGNASAGLNQVNNQGLTPLHLACQLGQEMVRVLL 240

QY 241 LCNARCNIMPNGYPTHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNIMPNGYPTHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300

QY 301 RMLLKGCVNNTSSAGNTALHGVNRRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCDVSTSSAGNTALHGVNRRPDCAIIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEMIKALIVGAEDVTDNDFGETPTFLASKIGR----- 395
DB 361 DNMVMKALIVGAEDVTDNDFGETPTFLASKIGR----- 395

QY 396 -----OLQDLAMHISPAKPAFILGSMRDEKETHD 425
DB 396 -----OLQDLAMHISPAKPAFILGSMRDEKETHD 425

QY 426 LLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRG 485
DB 426 LLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRG 485

QY 486 MYFRMKDEVFRGSRPYESGPLEBFLKREGEHTKMTDVKPKVMTGTTSDROPABELHLF 545
DB 486 MYFRMKDEVFRGSRPYESGPLEBFLKREGEHTKMTDVKPKVMTGTTSDROPABELHLF 545

QY 541 VYFRMKDEVFRGSRPYESGPLEBFLKREGEHTKMTDVKPKVMTGTTSDROPABELHLF 600
DB 541 VYFRMKDEVFRGSRPYESGPLEBFLKREGEHTKMTDVKPKVMTGTTSDROPABELHLF 600

QY 546 RNYDAPEVREPFNQNVLRLPQAQPSDOLVWAAESSGAAPYFRPNGRFLDGGILANN 605
DB 546 RNYDAPEVREPFNQNVLRLPQAQPSDOLVWAAESSGAAPYFRPNGRFLDGGILANN 605

QY 601 RNYDAPEVREPFNQNVLRLPQAQPSDOLVWAAESSGAAPYFRPNGRFLDGGILANN 660
DB 601 RNYDAPEVREPFNQNVLRLPQAQPSDOLVWAAESSGAAPYFRPNGRFLDGGILANN 660

QY 606 PTLDAMTEIHEYNQDLIRKQANKVKLSIVSLGTGRSPQVPVTCVDVFRSPNPWELAK 665
DB 606 PTLDAMTEIHEYNQDLIRKQANKVKLSIVSLGTGRSPQVPVTCVDVFRSPNPWELAK 665

QY 666 TVFGAKELGMVVDCCTDDPGR 687
DB 666 TVFGAKELGMVVDCCTDDPGR 742

RESULT 7
Q6DDKO PRELIMINARY; PRT; 756 AA.
AC Q6DDKO;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
```

OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Pancratic islets;
RM MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.,
RT "Pancratic islets express a Ca²⁺-independent phospholipase A2 enzyme
RT that contains a repeated structural homologous to the integral
RT membrane protein binding domain of ankyrin."
RL J. Biol. Chem. 272:11118-11127(1997).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
CC It has been implicated in normal phospholipid remodeling, nitric
CC oxide-induced or vasopressin-induced arachidonic acid release and
CC in leukotriene and prostaglandin production. May participate in
CC fas mediated apoptosis and in regulating transmembrane ion flux in
CC glucose-stimulated B-cells.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
CC heart and skeletal muscle.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U51898; AAC53136.1; -.
DR HSP; Q60778; LOY3.
DR RGD; 628867; Pla2g6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
FT REPEAT 348 377 ANK 7.
FT ACT_SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBBADA7FCC99B CRC64;
Query Match 90.2%; Score 3269.5; DB 1; Length 751;
Best Local Similarity 89.7%; Pred. No. 6.3e-241;
Matches 616; Conservative 30; Mismatches 40; Indels 1; Gaps 1;
QY 1 MQPFGRLVTFSGVTMLFSPNPRFKVAVADYTSDDRVREEGQLILFQNTPRTWDCVLV 60
DB 1 MQPFGRLVNTLSSTVTLFSPNPRFRAKESVADYASSERVREEGQLILQNASNRTWDCILV 60
QY 61 NPNRSQSGRLFOLEADALVNFHYSQSLLPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 SPNPSQSDRLFOLEADVNLVNFHYSQSLLPFYESSQVLHTEVLQ-LTDLIRNHPSW 119
QY 121 SVAHLAVELGIRCFHRSIIISNCAENEGCTPLHLACRGDGGILVELVQYCHTQMD 180
DB 120 TVTHLAVELGIRCFHRSIIITCANSTENEGCTPLHLACRGDSEILVELVQYCHQMD 179
QY 181 VTDYKGTVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPLHLACQLGQEMVRVLL 240
DB 180 VTDNKGETAFAHYAVQDNGSVQLLGRNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 239
QY 241 LCNARCNIWPGNYTHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAWA 300

Db 240 LCNARCNIWPGGPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAWA 299
QY 301 RMLLKRGCNNVNSTSAGNTALHVGVMRNFCAIVLLTHGANADARGHGNTPPLHLAMSK 360
Db 300 RMLLKRGCDDVSTASGNTALHVAVTRNRFDCVMVLLTYGANAGARGHGNTPPLHLAMSK 359
QY 361 DNVMIKALIVFGAEVDTPNDGGETPTLASKIGLOLDLMIHISPAKPAFTLGSMRDEK 420
Db 360 DNMEVKALIVFGAEVDTPNDGGETPTAFIASKISQLODLMPVSRARPAFTLSSMRDEK 419
QY 421 RTHDHLCLDGGVKGKLIILQLLIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKM 480
Db 420 RTHDHLCLDGGVKGKLIILQLLIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKM 479
QY 481 AYMRGMYFRMKDEVPFRGSRPYESGLPFLKREGEHTKMTDVRPKVMLTGLSDRQPA 540
Db 480 AYMRGMYFRMKDEVFRGSRPYESGLPFLKREGEHTKMTDVKPKVMLTGLSDRQPA 539
QY 541 ELHLFRNYDAPETVREPFRFNQNVNLRPPAOPSDQLVRAARSSGAAPTYFRPNGRFLDGG 600
Db 540 ELHLFRNYDAPEAVREPFRCTPNINUKPTQADQVLVRAARSSGAAPTYFRPNGRFLDGG 599
QY 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
Db 600 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKLSIVVSLGTGSKSPQVPTCVDFRPSNP 659
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
Db 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
RESULT 6
Q66HDI PRELIMINARY; PRT; 807 AA.
ID Q66HDI
AC Q66HDI; (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC081916; AAH81916.1; -.


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QY 541 ELHLFRNYDAPEVTRBPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRGFLDGG 600
Db 541 ELHLFRNYDAPEAVRPRCNQNLKPPTPQADQLVWRAARSSGAAPTFRPNRGFLDGG 600
QY 601 LIANNPTLDAMTEIHEYNODLRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
Db 601 LIANNPTLDAMTEIHEYNODLRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 660
QY 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 4
Q9JK61
ID Q9JK61 PRELIMINARY; PRT; 807 AA.
AC Q9JK61
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
GN Name-Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RA Chiu C.-H., Jackowski S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259401; AAF72651.1; -.
DR EMBL; BC057209; AAH57209.1; -.
DR HSSP; Q60778; 1OY3.
DR MGD; MGI:1859152; Pla2g6.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
```

```
KW ANK repeat.
SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match
Best Local Similarity 90.2%; Score 3271.5; DB 2; Length 807;
Matches 621; Conservative 31; Mismatches 35; Indels 55; Gaps 1;

QY 1 MQFFGRLVNTSGVNLFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTSLSSVTNLFNSNPRVKEVSLTDYVSSERVREEGQLILQNVSNRTWDCVLV 60
QY 61 NPNRSQSGFRLFOLELEADALVNFHYQSOLLPPFYESSQVLTHTVLOHLTDLIRNHPSW 120
Db 61 SPNPNQSGFRLFOLESEADALVNFQFSQLPFPFYESSQVLTHTVLOHLTDLIRNHPSW 120
QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRGDGEILVELVOYCHTOMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRGDSEILVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNPQVLQLGKNASAGLNVNNOGLTPLHLACKMGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKGCABMIISMDSQIHSKDPYRGASPLHWAKNAEA 300
Db 241 LCNARCNIMGPGFPPIHTAMKFSQKGCABMIISMDSNQIHSKDPYRGASPLHWAKNAEA 300
QY 301 RMLLRGCGNVNSTSAGNTALHVGWVRNPFCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRGCGDVTSSSGNTALHVAVMNRNFDCAIVLLTYGANAGARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFTGETPTFLASKIGR----- 395
Db 361 DNMEVVKALIVFGAEVDTNDFTGETPTFLASKIGR----- 420
QY 396 -----QLQDLMHISIRARKPAFILSSMRDEKSHDH 425
Db 421 VSTEQSSAAATHPLFSLDRTPAISLNLLEQLQDLMPISIRARKPAFILSSMRDEKSHDH 480
QY 426 LLCLDGGVGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRG 485
Db 481 LLCLDGGVGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRG 540
QY 486 MYFRMKDVEFRGSRPVESGPLEELKREFGHTKMTDVRKPKVMLTGTLSDRPAELHLF 545
Db 541 VYFRMKDVEFRGSRPVESGPLEELKREFGHTKMTDVRKPKVMLTGTLSDRPAELHLF 600
QY 546 RNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRGFLDGLLANN 605
Db 601 RNYDAPEAVRPRCNQNLKPPTPQADQLVWRAARSSGAAPTFRPNRGFLDGLLANN 660
QY 606 PTLDMATEIHEYNODLRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAK 665
Db 661 PTLDMATEIHEYNODLRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAK 720
QY 666 TVFGAKELGKMWVDCCTDPDGR 687
Db 721 TVFGAKELGKMWVDCCTDPDGR 742

RESULT 5
PA26 RAT
ID PA26 RAT STANDARD; PRT; 751 AA.
AC P97570;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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```
QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MOFFGRLVNTLSSVNTLFSNPRFVKEVSLTDYVSSRVEREGQLILLQNVSNRTWDCVLL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NPNRSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVLTHTVLOHLTDLIRNHPW 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SPNPSQSGFRLFOLESEADALVNFQFSQQLPPFYESSQVLTHTVLOHLTDLIRNHPW 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVOYCHTQMD 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDEILVELVOYCHAQMD 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VTDNKGETAFFHYAVQGDNPQVLLQGLKNASAGLNVNNOGLTPLHLACMGQEMVRVLL 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 LCNARCNIMGPNGYPIHSAKFQSGKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 LCNARCNIMGPGFPIHTAMKFSQKCAEMIISMDSNQIHSKDPYRGASPLHWAKNAEMA 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 RMLLKRCGCDVDSSTSSGNTALHVAVMNRFDCAIIVLLTVGANAGARGEHNTPLHLAMSK 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 DNVMKALIVFGAEVDTNDGETPTFLASKIGLOLQDLMIHSRARKPAFILGSMRDEK 420
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 DNMMVKALIVFGAEVDTNDGETPTPALIASISKLOLQDLMPISRARKPAFILSSMRDEK 420
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 RTHDHLCLDGGVKGVLIIQLLIAEKASGVATKDLFDWVAGTSGGILALAILHKSXM 480
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 421 RSHDHLCLDGGVKGVLIIQLLIAEKASGVATKDLFDWVAGTSGGILALAILHKSXM 480
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGHTKMTDVRPKVMLTGLSDRQPA 540
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 481 AYMRGVYFRMKDEVFRGSRPYESGPLEFLKREFGHTKMTDVKPKVMLTGLSDRQPA 540
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 3
Q7TPX2

```
ID Q7TPX2 PRELIMINARY; PRT; 752 AA.
AC Q7TPX2;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Loewen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusi D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAH52845.1; -.
DR HSSP; P07207; I078.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AAFC CRC64;
```

Query Match 91.1%; Score 3302; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 2.1e-243;
Matches 621; Conservative 30; Mismatches 36; Indels 0; Gaps 0;

```
QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MOFFGRLVNTLSSVNTLFSNPRFVKEVSLTDYVSSRVEREGQLILLQNVSNRTWDCVLL 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NPNRSQSGFRLFOLEADALVNFHQSOLLPPFYESSQVLTHTVLOHLTDLIRNHPW 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SPNPSQSGFRLFOLESEADALVNFQFSQQLPPFYESSQVLTHTVLOHLTDLIRNHPW 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVOYCHTQMD 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDEILVELVOYCHAQMD 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGQEMVRVLL 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VTDNKGETAFFHYAVQGDNPQVLLQGLKNASAGLNVNNOGLTPLHLACMGQEMVRVLL 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 LCNARCNIMGPNGYPIHSAKFQSGKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 LCNARCNIMGPGFPIHTAMKFSQKCAEMIISMDSNQIHSKDPYRGASPLHWAKNAEMA 300
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 RMLLKRCGCDVDSSTSSGNTALHVAVMNRFDCAIIVLLTVGANAGARGEHNTPLHLAMSK 360
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 DNVMKALIVFGAEVDTNDGETPTFLASKIGLOLQDLMIHSRARKPAFILGSMRDEK 420
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 DNMMVKALIVFGAEVDTNDGETPTPALIASISKLOLQDLMPISRARKPAFILSSMRDEK 420
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 RTHDHLCLDGGVKGVLIIQLLIAEKASGVATKDLFDWVAGTSGGILALAILHKSXM 480
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 421 RSHDHLCLDGGVKGVLIIQLLIAEKASGVATKDLFDWVAGTSGGILALAILHKSXM 480
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 AYMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGHTKMTDVRPKVMLTGLSDRQPA 540
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 481 AYMRGVYFRMKDEVFRGSRPYESGPLEFLKREFGHTKMTDVKPKVMLTGLSDRQPA 540
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
DR HSSP; Q60778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match          98.5%; Score 3572; DB 1; Length 806;
Best Local Similarity 92.4%; Pred. No. 5.2e-264;
Matches 685; Conservative 1; Mismatches 1; Indels 54; Gaps 1;

QY 1 MQFFGRLVNTFSVTNLFNSPFRVKEVAVADYTSDDVRREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSVTNLFNSPFRVKEVAVADYTSDDVRREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLELEADALNPHQVSSQLLPYESSPOVLHTEVLOHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLELEADALNPHQVSSQLLPYESSPOVLHTEVLOHLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRCFHHSRIISCANCAENEGCTPLHLACRKGDELVELVOYCHTQMD 180
DB 121 SVAHLAVALGIRCFHHSRIISCANCAENEGCTPLHLACRKGDELVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAWA 300
DB 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAWA 300

QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRDPDCAIVLLTHGANADARGEHGTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRDPDCAIVLLTHGANADARGEHGTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTPNDGFTPTFLASKIGR----- 395
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QY 396 -----QLQDLMIHSRARKPAFILGSMRDEKRTDHL 426
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QY 427 LCLDGGVKGILLIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 486
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QY 487 YFRMKDEVFRGSRPYESGPLEEFKREFGHTKMTDVKPKVMLTGTLSDRQPAELHLFR 546
DB 541 YFRMKDEVFRGSRPYESGPLEEFKREFGHTKMTDVKPKVMLTGTLSDRQPAELHLFR 600

QY 547 NYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGLLANNP 606
DB 601 NYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTFRPNRFLDGLLANNP 660

QY 607 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAKT 666
DB 661 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAKT 720

QY 667 VFGAKELGKMWVDCCTDPDGR 687
DB 721 VFGAKELGKMWVDCCTDPDGR 741

RESULT 2
PA26_MOUSE
ID PA26_MOUSE STANDARD; PRT; 752 AA.
AC P97819; Q991A9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Plaz2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RC STRAIN=DBA/2;
RX MEDLINE=97326816; PubMed=9079688; DOI=10.1074/jbc.272.13.8576;
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
RL P38D1 macrophages and Chinese hamster ovary cells.";
RN J. Biol. Chem. 272:8576-8580(1997).
RP [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RL Submitted [FEB-2000] to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
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DR HSSP; Q60778; 10Y3.
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DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
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DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
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FT REPEAT 185 215 ANK 2.
FT REPEAT 219 248 ANK 3.
FT REPEAT 251 281 ANK 4.
FT REPEAT 286 312 ANK 5.
FT REPEAT 316 345 ANK 6.
FT REPEAT 349 378 ANK 7.
FT ACT_SITE 465 465 Potential.
FT SEQUENCE 752 AA; 83702 MW; AAC3347B0E1292E9 CRC64;

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MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
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Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
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Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd O.M.,
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Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
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Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
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O'Brien K.P., Wilkinson P., Bodenreich A., Hartman K., Hu X.,
Khan A.S., Lane L., Tilahun Y., Wright H.;
"The DNA sequence of human chromosome 22.";
Nature 402:489-495(1999).
[7]
SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[1]
-!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
It has been implicated in normal phospholipid remodeling, nitric
oxide-induced or vasopressin-induced arachidonic acid release and

in leukotriene and prostaglandin production. May participate in
fas mediated apoptosis and in regulating transmembrane ion flux in
glucose-stimulated B-cells.
-!- FUNCTION: Isoform ankryrin-IPLA2-1 and isoform ankryrin-IPLA2-2,
which lack the catalytic domain, are probably involved in the
negative regulation of iPLA2 activity.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a carboxylate.
-!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
-!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
bound. Isoform SH-IPLA2 is cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
Name=LH-IPLA2;
IsoId=O60733-1; Sequence=VSP_000278;
Name=SH-IPLA2;
IsoId=O60733-2; Sequence=VSP_000278;
Name=Ankryrin-IPLA2-1;
IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
Name=Ankryrin-IPLA2-2;
IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
-!- TISSUE SPECIFICITY: Four different transcripts were found to be
expressed in a distinct tissue distribution.
-!- SIMILARITY: Contains 7 ANK repeats.

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or send an email to license@isb-sib.ch.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 111.829 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-23

Perfect score: 3625

Sequence: 1 MQFFGLVNTFGVTNLFNS.....GAKELGMVVDCTDPDGRP 688

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3572	98.5	806	1 PA26 HUMAN	O60733 homo sapien
2	3312	91.4	752	1 PA26 MOUSE	P97819 mus musculus
3	3302	91.1	752	2 Q7TPX2	O7tpx2 mus musculus
4	3271.5	90.2	807	2 Q9UK61	Q9jk61 mus musculus
5	3269.5	90.2	751	1 PA26 RAT	P97570 rattus norv
6	3267.5	90.1	807	2 Q66HD1	Q66hd1 rattus norv
7	2216	61.1	756	2 Q6DDK0	Q6ddk0 xenopus lae
8	1974	54.5	818	2 Q6NWO0	Q6nwy0 brachydanio
9	1165.5	32.2	879	2 Q7Q2U1	Q7q2u1 anopheles g
10	1165	32.1	877	2 Q9VT60	Q9vt60 drosophila
11	1165	32.1	887	2 Q7KUD4	Q7kud4 drosophila
12	741.5	20.5	386	2 Q8MR13	Q8mr13 drosophila
13	651	18.0	1071	2 Q20500	Q20500 caenorhabdi
14	6239	17.3	1023	2 Q62398	Q62398 caenorhabdi
15	622	17.2	1021	2 Q810Q6	Q810q6 caenorhabdi
16	453.5	12.5	762	2 Q95YD2	Q95yd2 caenorhabdi
17	350	9.7	501	2 Q9N5L3	Q9n5l3 caenorhabdi
18	338	9.3	843	2 P97582	P97582 rattus norv
19	338	9.3	1219	2 Q8C8R3	Q8c8r3 mus musculus
20	332	9.2	1863	2 Q723L5	Q7z3l5 homo sapien
21	332	9.2	3924	1 ANK2 HUMAN	Q01484 homo sapien
22	324	8.9	1004	2 Q7JUNZ0	Q7jnz0 caenorhabdi
23	324	8.9	1786	2 Q17344	Q17344 caenorhabdi
24	324	8.9	1809	2 Q17487	Q17487 caenorhabdi
25	324	8.9	1815	2 Q17488	Q17488 caenorhabdi
26	324	8.9	1841	2 Q8MQG0	Q8mqg0 caenorhabdi
27	324	8.9	1867	2 Q17486	Q17486 caenorhabdi
28	324	8.9	2039	2 Q17489	Q17489 caenorhabdi
29	324	8.9	6994	2 Q17343	Q17343 caenorhabdi
30	324	8.9	6994	2 Q17490	Q17490 caenorhabdi
31	319.5	8.8	1549	2 Q24241	Q24241 drosophila

32	319.5	8.8	1549	2 Q9V4B1	Q9vb1 drosophila
33	310.5	8.6	1501	2 Q7QKD3	Q7qkd3 anopheles g
34	310	8.6	1009	2 Q8SWY2	Q8swy2 drosophila
35	310	8.6	1159	2 Q9NCP8	Q9ncp8 drosophila
36	310	8.6	1571	2 Q7KU92	Q7ku92 drosophila
37	306	8.4	820	2 Q8JHU3	Q8jhu3 brachydanio
38	305.5	8.4	525	2 Q9TYS0	Q9tyso caenorhabdi
39	305.5	8.4	792	2 Q7Q172	Q7q172 anopheles g
40	301.5	8.3	786	2 Q9ERK0	Q9erk0 mus musculus
41	301.5	8.3	1136	2 Q9N180	Q9n180 bos taurus
42	299	8.2	1726	2 Q8VC68	Q8vc68 mus musculus
43	298	8.2	2622	2 Q70511	Q70511 rattus norv
44	297.5	8.2	1614	2 Q7TiG6	Q7ti96 brachydanio
45	296.5	8.2	1145	2 Q7PEZ8	Q7pez8 anopheles g

ALIGNMENTS

RESULT 1
PA26 HUMAN
ID PA26 HUMAN STANDARD; PRT: 806 AA.
AC O60733; O75645; Q8N452; Q9UC29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-
PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonyms=iPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND
ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=9079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent
phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancratic islets;
RX MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct
catalytically active isoforms of group VI phospholipase A2 (iPLA2)
that arise from an exon-skipping mechanism of alternative splicing of
the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616 (1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes
with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RA Ansonge W., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND
THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
Sherwood J.K., Sherwood A.M., Leichauser B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RT Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

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A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A;Reference number: PC2220; MUID:95071348; PMID:7526850
A;Accession: PC2220
A;Molecule type: protein
A;Residues: 910-929 <HER>
R;Davis, L.H.; Bennett V.
J. Biol. Chem. 265, 10589-10596, 1990
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A;Reference number: A35443; MUID:90285190; PMID:2141335
A;Accession: A35443
A;Molecule type: protein
A;Residues: 'X', '5', 'X', '7', '12', '403-417', 'X', '419-422', 'H', '424', 'LQ', '797-800', 'L', '802-814', '862-863',
C;Genetics:
A;Gene: GDB:ANK1; ANK
A;Cross-references: GDB:118737; OMIM:182900
A;Map position: 8p11.2-8p11.2
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C;Keywords: alternative splicing; phosphoprotein
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F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
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F;700-732/Domain: ankyrin repeat homology <AN21>
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F;828-1382/Region: spectrin binding
F;1383-1881/Domain: 55K #status predicted <DOM3>

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QY 107 LQHLTDLRNPHSWSVAHLAVELGIRECFPH--SRIISCANCAENE---EGCTPLHLACR 161
DB 336 LQHLTPEL-----HVAA-----HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIACK 380
QY 162 KGDGEILVELVQYCHTQMD-----VTDYKGET 188
DB 381 KKHVRVM-ELLTKTGASIDAVTESGTLPLHVSFMGHLPIVRKNLLQRGASPNVSNVKVET 439
QY 189 VFHYAVQGDNSQVLQLGRNAVAGLVNNOGLTPLHLACOLGKQEMVRVLLLCNARCN 248
DB 440 PLHMAARAGHTEVAKYLLQNK-AKVNAKAKDDQTLPHCARIGHTNMVKLLLENNANPNL 498
QY 249 MGPNGY-----PIHSAMKFSQKGCAMIIISM 274
DB 499 ATTAGHTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAKYKVRVAELLER 558
QY 275 DSSQIHSDPRYCASPLHWA---KNAEMARMLLKRCGNVNSTSSAGNTALHVGVMNRFD 331
DB 559 DAHP--NAAGKNGLTPLHVAHVHNNLDIVKLLPRGSPHSPAWNGYTPPLHIAAKQNOVE 616

QY 332 CAIVLLTHGANADARGEHGNTPHLHAMSNDVEMIKALIVFGAEVDTPNDFGTPTFLAS 391
DB 617 VARSLIQYGGSANABSVQGVTPHLHAAQEGHAEMVALLLSKQANGNLGNKSLTPLHLVA 676
QY 392 KIG 394
DB 677 QEG 679

Search completed: May 26, 2005, 14:20:39
Job time : 22.6953 secs

F;238-270/Domain: ankyrin repeat homology <AN07>

Biochem. Biophys. Res. Commun. 204, 453-460, 1994

1. RESEARCH AND DEVELOPMENT

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F:762-794/Domain: ankyrin repeat homology <AN22>
F:795-827/Domain: ankyrin repeat homology <AN23>

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Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;

Qy 124 HLAVELGIRECFHSHRIISCANCAENEGCTPLHLACRGDGBILVELVOYCHTQMDVTD 183
      ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 504 HISARLGKADIVQOLLQOGASPNAAITSGYTPLHLSAREGHEDVAAPFLDH-CASLSITT 562
      ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 184 YKGETVFHYAVQDGNQSVQLLGRNAVAGLVQNNQGLTPLHLACOLGKQEMRVVLLCN 243
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 563 KKGFTPLHAAKYGKLEIVANLLQKS-ASPDAAAGKSGLTPLHVAAHYDQKVALLLDQG 621
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 244 ARCNIMGPNGY-PIHSAMKFSQKGAEMII--SMDSSQHSKDPRYGASPLHWAK---NA 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 ASHPAAAKNGYTPLHIAAKNQMDIATLLEYCADANAV----TROGIASVHLAAQEGHV 677
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 298 EMARMLLKRCGNVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHGTPLHLA 357
      ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 678 DMVSLLLGRNAVNNLNKSLGTLPLHLAAQEDRVNVAEVLVNQGAHVDAQTCKMGYTPLHVG 737
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 358 MSKDNVEMIKALIVGAQVDTPNDFGTTFTFLASKIG 394
      ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 738 CHYGNIKIVNLFLLQHSKAKVNAKTKNGYTPLHQAAQQG 774
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
B35049
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N:Contains: ankyrin 2.2, erythrocyte
C:Species: Homo sapiens (man)
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C:Accession: B35049
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370; PMID:1689849
A:Accession: B35049
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1856 <LAW>
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
F:2-1533,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>

```


C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

R;Accession: T42715
R;Species: L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995

A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.

A;Reference number: Z22237; MUID:95340633; PMID:7615634

A;Accession: T42715

A;Status: preliminary; translated from GB/EMBL/DDB

A;Molecule type: mRNA

A;Residues: 1-1940 <PET>

A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

A;Experimental source: strain C57BL/6J; kidney

C;Genetics:

A;Gene: Ank3

A;Map position: 10

A;Introns: 834/1

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing

Query Match 8.2%; Score 296; DB 2; Length 1940;
Best Local Similarity 24.7%; Pred. No. 2.7e-14;
Matches 112; Conservative 82; Mismatches 191; Indels 68; Gaps 18;

Qy 124 HLAVELG----IRECFHSHRIISCANCAENEECTPLHLACRGDGEILVELVOYCHTQM 179
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 421 HVAAFMGHVNVISQLMH-----GASPNNTTVRGETALHMAARSGQAEVVRYLVQ-DGAQV 475
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 180 DVTDYKGETVFHYAVQGDNSOVLLQGLGRNAVAGLNQNNQGLTPLHLACOLGKQEMVRVL 239
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 476 EAKAKDDQTPLHLSARLGKADIVQOLLQQG-ASPNAATTGGYTPLHLAREGHEDVAEFL 534
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 240 LLCNARCINMGPGY-PIHSAMFQSQKGCACMIISMDSSQIHSKDPTRYCASPLHWA---K 295
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 535 LDHGASLSITTKGFTPLHVAAKYGVLEVASLLLOKSASP--DAAGKSLGPLHVAHYD 592
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 296 NAEWARMLLKRCGNVNSTSGANTALHVGVMNRFPDCAIVLLTHGANADAARGHGNTPHL 355
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 593 NQKVALLLLDQGASPHAAKNKGTYPLHIAKKQMDIATSLLEYGADANAATVQTGIASVH 652
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 356 LAMSKNVEMIKALIVEGASVDTPNDPGETPTFLASKIGR-QLQDLM-----HISRARKP 409
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy .653 LAAQEGHVDWMSULLSRNANVLNKSGLTPLHLAAQEDRVNVAEVLVNGQAHVDAOTKM 712
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 410 AFILGSNRDEKRTHDLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTGTGGI 469
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 713 GY-----TPLHVC-C-HYGNIK---IVNFLLQHSACKVNAKTQN-----GY 747
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 470 LAAILHKSMAVYRMGMFRMKDEVFGSRPYE---SGPLEEFLLKRFEGHTTQMTDVVK- 525
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 748 TAL-----HQAQQOQHITHIINVLLQNNASPNELTVNGNTALAIARRLG-YISVVDTLKV 800
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 526 --PKVMLTGILSDROPALHLFRNYDAPEVRE 556
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

Qy 801 VTBEIMTTTTITEK-----HKMNVPETMNE 825
Db |||::||::||::||::||::||::||::||::||::||::||::||::||::||:
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604

RESULT 10
T42713
ankyrin 3, splice form 1 - mouse
C;Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42713
R;Species: L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995

A>Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene the repeat domain.

A;Reference number: Z22237; MUID:95340633; PMID:7615634

A;Accession: T42713

A;Status: preliminary; translated from GB/EMBL/DDB

A;Molecule type: mRNA

A;Residues: 1-1943 <PET>

A;Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710550; PIDN:AAB01604

Qy	499	RPYESGPLEEFLKRFEGHGTQMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVRPR	555
Db	703	-----PVAQILYNNGAEINSGTKNAGTYTFLHVACHFGQLNMVYKFLVENGADYGEKTRA--	754
Qy	559	FNQVNLRPAPQSDQLVRAARSSGAAPTFRPNGRFLDGLGLANNPTLDAWTEIHEYN	618
Db	755	--SVTPLHQAAQQGHNNCVRYLLENGASP-----NEQTATGQTPL-----	792
Qy	619	QDLIRKGANKVKKLSIVVSLGTGRSPOV--PVTCDV-FRPSNPWELAKTVFGAKE	672
Db	793	-----SIAQRLGVSVVETLRTVTETVITETTTVDERYKPNQPEANMETWFSSE	843
RESULT 7			
T13940			
ankyrin - fruit fly (<i>Drosophila melanogaster</i>)			
C:Species: <i>Drosophila melanogaster</i>			
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004			
C:Accession: T13940			
R:Dubreuil, R.R.; Yu, J.			
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994			
A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in			
A:Reference number: Z17820; MUID:95024098; PMID:7937942			
A:Accession: T13940			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-1549 <DUB>			
A:Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:g557083; PID:g557084; PID:			
C:Genetics:			
A:Cross-references: FlyBase:FBgn0011747			
Query Match 8.8%; Score 319.5; DB 2; Length 1549;			
Best Local Similarity 22.3%; Pred. No. 2.7e-16;			
Matches 139; Conservative 80; Mismatches 180; Indels 223; Gaps 22			
Qy	45	ILFQNTNRTWDCVLVNPNSQSGFRLQLELEADALVNPHEYSSQLL-----PFYESSP	99
Db	319	LLOQNA-----ILTKNGLSALHM-----AAQGEHDEAAHLLDKNKAPVDEVTV	364
Qy	100	QVL-----HTEVLOHLLDLIRNHPS-----WSVAHLA-----VELGIRECFH	136
Db	365	DYLTALHVAACHGVKVAKLDDYKANPNARAINGFTPLHIACKNRKIMVELLIK---H	421
Qy	137	HSRIISCANCAENBEGCTPLHACKRGDEILVELVYCHTQMDVTDYKGTVFHYAVQG	196
Db	422	GANI-----GATTESGLTPLHVASPMGCINIVILLOH-EASADLPTIRGETPLHLAARA	475
Qy	197	DNSQVQLQLGNV-----	210
Db	476	NOADIIRLLRSKAVDAIVREGQTPLVASRLGNINIIMLLHQGAENIAOSNDKYSALH	535
Qy	211	-----AGLNQVNNQGLTPLHLHACQLGKQEMVRVLLLCNARCINMGPN	252
Db	536	IAAKEGQENIVQVLLLENGAENNAVTKGFTPLHACKYQNVVQILLQNGASIDFGQK	595
Qy	253	GY-PIHSAMKFSQKCAEMISMOSS-----QI--HSKD-283	
Db	596	DVTPLVATHYNNPNSIVLELLKNGSSPNLCARNGQCAITHACKKNYLEIAMOLLOHGADV	655
Qy	284	--PRYGASPLHWAK--NASEMARMLKRGCVNNTSSAGNTALHVGVMRNFDCAIULL	337
Db	656	NIISKSGFSPHLHAAQGNVDVWQLLEVG-ISAANKGLTPLHVAAQEGHVLVSQILL	714
Qy	338	THGANADARGHGNTPLHLAMS KONVEMI KALIVFGAEVDPNDPFGETPTFLASKIGRQL	397
Db	715	EHGANISERTNGYTPLHMAAHYGHLDLVKPFENDADIEMSSNIGYTPLHQAAQQGH--	772
Qy	398	QDLMHI SPARKPAFILGSMRDEKRTDHLHLLCDGGGVKGLIIQLLIAIEKASGVATKDL	457
Db	773	-----IMIINULLLRHKANPNALTKD-----	792
Qy	458	PDWVAGTSTGGILALAILHLSKSMAY--MRGMGYPRMKDDEVFRGSRPYSGPLEEFLKREF	514

[illegible]

```
RESULT 5
T33857
hypothetical protein D1037.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33857
R:Ledwith, J.; Biewald, T.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of C. elegans cosmid D1037.
A:Reference number: Z21424
A:Accession: T33857
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-468 <LED>
A:Cross-references: EMBL:AF106592; PIDN:AAC78490.1; GSPDB:GN00019; CESP:D1037.5
A:Experimental source: strain Bristol N2; clone D1037
C:Genetics:
A:Gene: CESP:D1037.5
A:Map position: 1
A:Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match          9.0%; Score 326; DB 2; Length 468;
Best Local Similarity 27.3%; Pred. No. 1.3e-17;
Matches 111; Conservative 74; Mismatches 164; Indels 58; Gaps 16;

QY 286 YGASPLHMAKNAEMARMMLKRGCNVNSTSSAGNTALHVGVMRN-----RFDCAIVLLTHG 340
DB 44 YDLSVITWLQN---LRFLLSRYCR-----SENVCNHLEALNAARYGNTDLLYKLYIH 94
QY 341 ANADARGEHNTPLHLAMSKNVEMIKALIVGAEVD---TNDFGETPTFLAS--KIGR 395
DB 95 IDLRMTDETGTAMHVAVMNNOQKIVRLVVLCAPCQIWKIKNNNGLTSTELCTDKKISE 154
QY 396 QIQDLMLHISRKAPAF-----ILGSMRDEKTRHDH-LLCLOGGGVKGKLIILQILIA 445
DB 155 DFKSLDNPPSPGAFVDVSEYNNVLAASEKQWPEERVLALDGGGIRAVITIQMLIH 214
QY 446 IEKASGVATKDLFDWVAGTSTGGILALAI-LHKSVMYMRGMVFRMKDEVF-RGSR---P 500
DB 215 IDYLLGGKLVKLDIDAGTSCGVITLLASTNNRIETRKLLDMRDVRVIRGADKAVP 274
QY 501 YESGPLEPLKEFP--GEHTKMTDVVKPKVMTLGTLSDRQPAELHLFRNY--DAPETVRE 556
DB 275 KYSSNGMEYIARHVITTWEDSKMSSIKRRAIVTVADTRMVPQQLLIFRSYRPEMPEACE 334
QY 557 P-RENOVNLRPPAOPSDQLVRAARSSCAAPTYRPNGRFLDGGILANNPTLDAMTEIH 615
DB 335 HYKF-----LDPTKVELWTKRLCTTAAPYFFPESFNGLSDDGGLIANNPTLALISDPF 385
QY 616 EYNQDLIRKQANKVK-----KLSIVVSLGTGRSPQVPVTCVDV 654
DB 386 LTNK--LEKSFAKSSSERENRGNWKIGCVISLGTGVFPTEKIDIDL 430

RESULT 6
T15347
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
R:Gattung, S.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid B0350.
A:Reference number: Z18332
A:Accession: T15347
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2039 <GAT>
A:Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA934
A:Accession: T15346
A>Status: preliminary; translated from GB/EMBL/DBJ
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A:Molecule type: DNA
A:Residues: 1-1000,'SKLQHRT',1002-1718,'KWEELNRL',1727,'D','ES',1942,'PSPAQRS',1950,'I'VAI
32,'S',2034-2035,'GSPTRRSVEPEHRHSQHEHGST' <GA2>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA934445.1
A:Accession: T15344
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718,'KW',1903-1905,'NRLADESPS',1916-1917,'QRSTIVASTSEQVPE',1934-1935,'E'
<GA3>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA934444.1
A:Accession: T15345
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718,'KWEELNRL',1727,'D','ES',1942,'PSPAQRS',1950,'I'VAERS',1956-1957,'EQVPE
PTRRSVEPEHRHSQHEHGST' <GA4>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA934446.1
R:Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpoor
J. Cell Biol. 129, 1081-1092, 1995
A:Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Caer
A:Reference number: A57282; MUID:95263663; PMID:7744957
A:Accession: A57282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852,'GGG',856-1000,'SKLOHRT',1002-1319,'IG',1322-1595,'DA',1598-1718,'KWEEL
',SHRED',2007-2008,'TI',2011,2017,'TT',2020-2022,'SHIS' <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: B57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852,'GGG',856-1319,'IG',1322-1595,'DA',1598-1718,'KWEELNRL',1727,1799,'E'
V',1945-1947,'VT',1950,'SH',1975,'SESP',1980-1981,'GPTRRSVEPEHRHS',1984-1985,'EDHEGS',19
4,'TIV',1828,'ESTS',1833,'QV',1836,'E',1934-1935,'ES',1939,'SES',1944,'REDDGITVTT',194
A:Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
C:Genetics:
A:Gene: CESP:unc-44
A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1799/
C:Superfamily: ankyrin; ankyrin repeat homology
F:164-192/Domain: ankyrin repeat homology <AN04>
F:358-390/Domain: ankyrin repeat homology <AN04>
F:391-423/Domain: ankyrin repeat homology <AN11>

Query Match          8.9%; Score 324; DB 2; Length 2039;
Best Local Similarity 24.0%; Pred. No. 1.8e-16;
Matches 129; Conservative 77; Mismatches 207; Indels 124; Gaps 16;

QY 147 AENEBCGTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLLG 206
DB 420 ATTESGLTPLHVAAPMGAINIVLYLQQ-GANPDVETVRGETPLHLAARANTDVVRVLI 478
QY 207 RNAVAGLNQVNOGLTPLHLACOLGKQEMVRVLLLCNARCNTGPNGY-PIHSAMKFSQK 265
DB 479 RNG-AKVDAQARELQTPHLIASRLGNTDIVILLQAGANSNATTRDYNVSPLHAAKEGOE 537
QY 266 GCAEMIISMDSQIHSKD----PRYGASPLHWAK---NAEMARMMLKRGCNVNSTSSAGN 318
DB 538 EVAGLLED-----HNADKTLTKGFTPLHLASKYGNLEVVRLLETRGTPVDIEGKNQV 591
QY 319 TALHGVVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSNDNVEMIKALIVFGAEVDT 378
DB 592 TPLHVAAHYNDKVAAMLLLENGASAKAAAKNGYTPHLIAAKKNQMEIASTLLQFKADPNA 651
QY 379 PNDFGETPTFLASKIGRQLQDLMLHISRKAPAFILGSMRDEKTRHDHLLCLDGGGVKGLI 438
DB 652 KSRAGFTPLHLSAQEGHK-----ANNGLTAMHLIC-----EISGLL 675
QY 439 IQQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSVMYMRGMVFRMKDEVFRGS 498
DB 676 -----IENGSDVGAK-----ANNGLTAMHLIC-----AQEDHV----- 702
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Db 425 PIIAMKRGKLDVSLRKMLEKQDGLTETPTTGNVTIHCANKKCLILIMKFRDQTD 484
QY 310 VNSTSGAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
Db 485 PEARNALQOTPLTFYIKDGLGVLWILSAYGVMDAQDINGNTPLHCAVTRGNTETARM 544
QY 370 IVFGAEVDTNDFGETPTFLASKI----- 393
Db 545 LCLGAKPDINKRYKESPRHIAARLTKKEAKWIDIVRALIICGAGACDDGFGICAFGCMWHT 604
QY 394 -----GRLOQL---MHIS--RARKP-AFILG-----SMRDKRT 422
Db 605 GLTSCKTQLGSSSDSQSMEDVRKDIHVSNDAAAPYEFVLDPTQLVEBAYARNETRA 664
QY 423 HDH-----LCLDGGGVKGLIIIIQLLIAIEKASGVATKDL 457
Db 665 FPHEALKRVNKLKELVEKKTSNVINVLGGGGIRGLVTVQMLICLEAFIDRLPIDY 724
QY 458 FDWVAGTSTGGILALAILHSKSMAYMRGMVFRMKDEVFRG-SRPYSGPLLEFLKREFGE 516
Db 725 FDIWIGATSTGYIMSTWMTGSLRKAQRYVLMFKDQLFDSWTRPYDTKTLETFIQARFGA 784
QY 517 HTKMTDVVRKPKVMTGLTSLDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 576
Db 785 DRLMGDIKYPRFCTTVRADTFPVQLELLNRYLRPISEKE---NNDLGF---TDPNELTI 838
QY 577 WRAARSSGAAPTFRN-GRFLOGGLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSI 635
Db 839 WKATRSSAAPTFYFSAEGFIDGGMISNNPVLIDMSDIGFYNTTCQMRIPKVMVDMGC 898
QY 636 VVSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFCAKELGRMVVDCCTDPDGRP 688
Db 899 VLSVGTGITPCVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATEGAP 947

RESULT 4
S37431
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N;Contains: ankyrin 2, short form
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text change 09-Jul-2004
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
R;Chan, W.
submitted to the EMBL Data Library, September 1993
A;Reference number: S37431
A;Accession: S37431
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-3924 <CHA>
A;Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g4062
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A;Reference number: A39643; MUID:91302466; PMID:1830053
A;Accession: A39643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2077 <OTL>
A;Cross-references: GB:X56957
A;Accession: B39643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1443,3585-3924 <OTT>
A;Cross-references: EMBL:X56958
R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
Genomics 10, 858-866, 1991
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A;Reference number: A40334; MUID:92009921; PMID:1833308
A;Accession: A40334
A;Molecule type: DNA
A;Residues: 463-474,'PE',477-495 <TSE>
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A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648
R;Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A;Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and se
A;Reference number: A49462; MUID:94075409; PMID:8253844
A;Accession: A49462
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-3924 <REG>
A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
C;Genetics:
A;Gene: GDB:ANK2
A;Cross-references: GDB:127607; OMIM:106410
A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
F;63-95/Domain: ankyrin repeat homology <AN01>
F;96-128/Domain: ankyrin repeat homology <AN02>
F;129-161/Domain: ankyrin repeat homology <AN03>
F;162-190/Domain: ankyrin repeat homology <AN04>
F;191-223/Domain: ankyrin repeat homology <AN05>
F;232-264/Domain: ankyrin repeat homology <AN06>
F;265-297/Domain: ankyrin repeat homology <AN07>
F;298-330/Domain: ankyrin repeat homology <AN08>
F;331-363/Domain: ankyrin repeat homology <AN09>
F;364-396/Domain: ankyrin repeat homology <AN10>
F;397-429/Domain: ankyrin repeat homology <AN11>
F;430-462/Domain: ankyrin repeat homology <AN12>
F;463-495/Domain: ankyrin repeat homology <AN13>
F;496-528/Domain: ankyrin repeat homology <AN14>
F;529-561/Domain: ankyrin repeat homology <AN15>
F;562-594/Domain: ankyrin repeat homology <AN16>
F;595-627/Domain: ankyrin repeat homology <AN17>
F;628-660/Domain: ankyrin repeat homology <AN18>
F;661-693/Domain: ankyrin repeat homology <AN19>
F;694-726/Domain: ankyrin repeat homology <AN20>
F;727-759/Domain: ankyrin repeat homology <AN21>
F;760-792/Domain: ankyrin repeat homology <AN22>
F;793-825/Domain: ankyrin repeat homology <AN23>
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Query Match 9.2%; Score 332; DB 2; Length 3924;
Best Local Similarity 27.3%; Pred. No. 1.2e-16;
Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;
QY 103 HTEVLOHLD-----LIRNHPSSWVAHLAVELGIRCFHH-----SRIL 141
Db 311 HDQVVELLERGAPLLARTKNGLSPLHMAAQGDHVECVKHLLOHKAQPVDDVTLDYLTALH 370
QY 142 SCANC-----AENEEGCTPLHLACRKGDEILVELVOY----- 174
Db 371 VAHGHYRVTKLLDKRANPNARALNGFTPLHIACKNRKIKWELLVKYTGASIQAITES 430
QY 175 ----CH-----TOMDVTYKGETVFHYAVQGDNSQVLLQLEGRNAVAG 212
Db 431 GLTFPIHVAAPMGHLNIVLLQLQNGASPDVTNIRGETALHMAARAGQVEVVRCLLRNG-AL 489
QY 213 LNQVNNQGLTPLHLACQLQKQEMVRVLLLCNARCNITMGNGY-PIHSAMKFSQKGCHEMI 271
Db 490 VDAARAREQTPLHIASRLGKTEIVQLLQHMAHPDAATNGYTPHLHISAREGOVDVASVL 549
QY 272 ISMDSQIHSKOPRYCASPLHWAK---NAEMARMKLKRCNVNNTSSAGNTALHVGVMRN 328
Db 550 --LEAGAAHSLATKKGFTPLHVAANKYGSIDLVAKLLQRAAADSAGKNGTTPHLHVAHYD 607
QY 329 RFDCAIVLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDFGETPTTF 388
Db 608 NQKVALLLLEKSGASPHATAKNGYTPHLHIAAKNQMOIASTLLANYGAETNIVTKQGVTPFH 667
QY 389 LASKIG 394
Db 668 LASQEG 673
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Db 466 VPAEQSAAPHFSSLERAQPPISLNLEQLDLMIHSPARKPAFILGSMRDEKTRTHDL 525
QY 427 LCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGM 486
Db 526 LCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGM 585
QY 487 YFRMKDEVFRGSRPYESGPLEBFLKEEFGHTKMTDVRPKVMTGTLSDRQPAELHLFR 546
Db 586 YFRMKDEVFRGSRPYESGPLEBFLKEEFGHTKMTDVRPKVMTGTLSDRQPAELHLFR 645
QY 547 NYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSAGAAPTYFRNGRFLDGLLANNP 606
Db 646 NYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSAGAAPTYFRNGRFLDGLLANNP 705
QY 607 TLDAMTEIHEYNQDLIRKQOANKVKLSIVVSLGTRSPQVPVTCVDVFRPNPNWELAKT 666
Db 706 TLDAMTEIHEYNQDLIRKQOANKVKLSIVVSLGTRSPQVPVTCVDVFRPNPNWELAKT 765
QY 667 VFGAKELGRWVDDCCTDPDGR 687
Db 766 VFGAKELGRWVDDCCTDPDGR 786

RESULT 2
T22327
hypotheical protein F47A4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22327
R:Mortimore, B.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19549
A:Accession: T22327
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1071 <WIL>
A:Cross-references: UNIPROT:O20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN000028; CESP:F47A4
A:Experimental source: clone F47A4
C:Genetics:
A:Gene: CESP:F47A4.5
A:Map position: X
A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 18.0%; Score 651; DB 2; Length 1071;
Best Local Similarity 27.1%; Pred. No. 1.1e-42;
Matches 195; Conservative 125; Mismatches 260; Indels 140; Gaps 20;

QY 69 FRLFOLELEADALVNFHQYSSQLLPYESSQVLTHTVL----QHLTDLIRNHPNSVAH 124
Db 315 FSLFRATDKKDLMLLHLCDEKSFLLTSLDMTMRADILRSKIEELVIOIRLKPHYHMT 374
QY 125 LAVELGIRECFHHSRI-----ISCANCAENBEGCTPLHLACRKGDGELVELVOY 174
Db 375 VAIAITDRDLDFSDGMKTKWNETLEPPESQLRCLCHTENCYPHALTMDROKIVERLLEL 434
QY 175 CHTQMDVTDYKGETVPHYAVQGDNSQVQLLGRNAVAG---LNQVNNQGLTFLHLACQGL 231
Db 435 DPTLFCETKAGNVVHHV---NSSFCAQIIWDRCPASQHFIDERNMDCQSPLEAVSTA 491
QY 232 QBMVRVLLLCNARCINMGPNGYPHSAKMFQKQCAEMIISM-----DSS 277
Db 492 KPLVATFL-----LKGAKFTRGDRNELFVAMTSKNAQSVVEVLTDRK 535
QY 278 QIHSKDPYRCASPLHWAKNAEMARMLLR-----GCNVNSTSAGNTALHVGVMRNFPCA 333
Db 536 EIANERDALGNSAIIHVALYKESINALLNKRVELGLDIDVKNAGETALLFITTRKPDLL 595
QY 334 IVLLT---HGANADARGEHNTPLHLAMS-----KDNVEMIKALIVFGAEVDPNDFGST 385
Db 596 PLLVTLYHAGANNATDPGNTALHKSAAALVDAKKISLECVKFLISAGSNPNKINLRGES 655
QY 386 PTFLASKIGROLQDLWHISRA---RKPAFILG-----SMRDE-----419

Db 656 PRHLAASL--QNQEMLAAILKAAATRCPKGYKGCSCNCRHDCSSABDEYEETLQKIRIGN 713
QY 420 -----KRTDHLCLDGGVKGGLIIQLLIAIEKASGV 452
Db 714 ESDYEKTEFTASEKLNIOQTLDSSRRGKKAKVNLISMDGGGIRGLVLIOTLAIERLGD 773
QY 453 ATKDLFDWVAGTSTGGILALAILHLSKSMAYMRGMFRMKDEVFRG--SRPYESGPLEEFLUK 511
Db 774 DIFKTFDMSAGTSTGSLIMAGLATKSLREMQOQTYLLKDRVFDGIMPYDVTVOLEKFTQ 833
QY 512 REFQGHKTMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOP 571
Db 834 DQFGTGT--VWEIPYPRLMISAVNSEKLPVRLMARNYKPAKV-----APETP 880
QY 572 SDQLVWRAARSAGAAPTYFRPN--GRFLDGLLANNPTLDMATEIHEYNQDLIRKQOANKV 630
Db 881 KEMPLWALRRSTAAPVLFKPSDEDRYIDGGIISNNPALDLMSEVHAYNRELQSGRKSDA 940
QY 631 KKLISIVVSLGTRSPQVPVTCVDVFR--PSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 688
Db 941 VQMNVLVSFGTG---QIFSTVIETLSIDSNSPLQSIKTI---KNLAAMFIDQATASEGAP 994

RESULT 3
T26261
hypotheical protein W07A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26261; T26892
R:Baeham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20184
A:Accession: T26261
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1023 <WIL>
A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CAB04932.1; GSPDB:GN000023; CESP:W07A8.2
A:Experimental source: clone W07A8
R:Ainscough, R.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20281
A:Accession: T26892
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1023 <WIL>
A:Cross-references: EMBL:AL021489; PIDN:CAA16371.1; GSPDB:GN000023; CESP:W07A8.2
A:Experimental source: clone Y44A6C
C:Genetics:
A:Gene: CESP:W07A8.2
A:Map position: 5
A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 708/3

Query Match 17.3%; Score 627; DB 2; Length 1023;
Best Local Similarity 23.9%; Pred. No. 8.2e-41;
Matches 185; Conservative 153; Mismatches 285; Indels 150; Gaps 23;

QY 37 RVREBQGLILFQNTPNRTWDCVLPNPRNSQSGFRILFQLELEAD--ALVNFHQYSSQLLPF 94
Db 204 RAKEBEEL--KNKELYHLAITYLNENNEKYVMSLFRSHKLADVVALCERCENPELPRV 260
QY 95 YESSQV---LHTEVLQHLTDLIRNHPNSVAHLAVELGIRECFHH---SRIISCANCAE 148
Db 261 FPKNNYNIKDYLT-----IFHELNDNTWKSVHISISKIGLLEYFENMEKHLKKLYNLIV 315
QY 149 NEEGCTPLHLACRKGDELVELVOYCHTQMDVTDYKGETVPHYAVQGDNSQVQLL--G 206
Db 316 QPEGUSPLMIAVQNTQIETVSNMLDH--GADINILSSEQQNVLHVAATASSGDLIKILNET 374
QY 207 RNAVAGLNQVNNQGLTFLHLACOLGQKQBMVRVLLLCNARCINMGPNG-----Y 254
Db 375 KKCETMINQTSNGYTPAYVA-----LINACLNCQTLRGFGGIGQSSDSTOMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMARMMLLR---GCN 309

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 19.6953 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-23
Perfect score: 3625
Sequence: 1 MQFFGRLVNTFSGVTNLFN.....GAKELGKMVVDCTDPDGRP 688

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3572	98.5	851	T12503	hypothetical prote
2	651	18.0	1071	T22327	hypothetical prote
3	627	17.3	1023	T26261	hypothetical prote
4	332	9.2	3924	S37431	ankyrin 2, neuroma
5	326	9.0	468	T33857	hypothetical prote
6	324	8.9	2039	T15347	ankyrin-related un
7	319.5	8.8	1549	T13940	ankyrin - fruit fl
8	296	8.2	1765	T42714	ankyrin 3, splice
9	296	8.2	1940	T42715	ankyrin 3, splice
10	296	8.2	1943	T42713	ankyrin 3, splice
11	296	8.2	1961	T42716	ankyrin 3, splice
12	296	8.2	4377	T45575	ankyrin 3, long sp
13	294	8.1	1856	T35049	ankyrin 1, erythro
14	294	8.1	1880	T35049	ankyrin 1, erythro
15	294	8.1	1881	1 SJHUK	ankyrin 1, erythro
16	287	7.9	1862	T49502	ankyrin - mouse
17	285	7.9	1848	T37771	ankyrin, erythrocy
18	282	7.8	397	T46445	hypothetical prote
19	273	7.5	1265	T02131	hypothetical prote
20	273	7.5	1411	T30355	alpha-latroinsecto
21	269.5	7.4	456	T24442	hypothetical prote
22	263.5	7.3	1423	T37275	death-associated p
23	249	6.9	791	T42691	hypothetical prote
24	248.5	6.9	1435	T32930	hypothetical prote
25	244	6.7	247	T08448	probable ankyrin l
26	239	6.6	426	T42149	hypothetical prote
27	237	6.5	1401	T11527	alpha-latrotoxin p
28	236	6.5	368	T18184	ankyrin repeat pro
29	236	6.5	2437	T42612	transmembrane prot

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFPz434A102.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Accession: T12503
R;Ansoerge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17527
A;Accession: T12503
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-851 <NS>
A;Cross-references: EMBL:AL080187
A;Experimental source: adult testis; clone DKFPz434A102
C;Genetics:
A;Note: DKFPz434A102.1

Query Match	98.5%	Score	3572	DB	2	Length	851
Best Local Similarity	92.4%	Pred. No.	5.2e-273				
Matches	685	Conservative	1	Mismatches	1	Indels	54
Gaps							1
QY	1	MOFFGRLVNTFSGVTNLFNPPRVKEVAVADYTS	DRVREEGQLILFQNTPNRTWDCVLV	60			
DB	46	MOFFGRLVNTFSGVTNLFNPPRVKEVAVADYTS	DRVREEGQLILFQNTPNRTWDCVLV	105			
QY	61	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLP	PFYESSQVLTHTVQLHQLTDLIRNHPSW	120			
DB	106	NPRNSQSGFRLFQLELEADALVNFHQYSSQLLP	PFYESSQVLTHTVQLHQLTDLIRNHPSW	165			
QY	121	SVNHLAVELGIRECFHHSRIISCANCAENEGCT	PLHLACRKGDELIVELVOYCHTQMD	180			
DB	166	SVNHLAVELGIRECFHHSRIISCANCAENEGCT	PLHLACRKGDELIVELVOYCHTQMD	225			
QY	181	VTDYKGETVFHVAVQDQNSQVLQLGRNAVAGLN	QVNNQGLTPLHLACQLGKGEWVRVLL	240			
DB	226	VTDYKGETVFHVAVQDQNSQVLQLGRNAVAGLN	QVNNQGLTPLHLACQLGKGEWVRVLL	285			
QY	241	LCNARCINMGPNGYPIHSAKFSSQKCAEMIIIS	MDSSSQIHSKDPRYGASPLHWAKNAEMA	300			
DB	286	LCNARCINMGPNGYPIHSAKFSSQKCAEMIIIS	MDSSSQIHSKDPRYGASPLHWAKNAEMA	345			
QY	301	RMLLKGCNNVNTSSAGNTALHVGWVRNRPDCAI	VLTLTHGANADARGEHGTPLHLAMSK	360			
DB	346	RMLLKGCNNVNTSSAGNTALHVGWVRNRPDCAI	VLTLTHGANADARGEHGTPLHLAMSK	405			
QY	361	DNVEMIKALIVFGAEVDVTNDFGETPTFLASKIG	R-----	395			
DB	406	DNVEMIKALIVFGAEVDVTNDFGETPTFLASKIG	R-----	465			
QY	396	-----	QLQDLMIHSRARKPAFILGSMRDEKRTDHL	426			

QY 241 LCNARCNMGNGYPIHSAMKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAMKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG- LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG- LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDLHLLCLDGGVGLIIQIIILIAIEKASGVATKDLFDWVAGTSTGGTILALAILHSKSM 479
DB 421 RIHDLHLLCLDGGVGLVIQIIILIAIEKASGVATKDLFDWVAGTSTGGTILALAILHSKSM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRPKVWMLTGTLSDROPA 539
DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRPKVWMLTGTLSDROPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQLVWRAARSSGAAPTFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQLVWRAARSSGAAPTFRPNRFLDGG 600
QY 600 LIANPPTLDAMTEIHEYNQDLIRKGOANKVKLSIIVSLGTRSGRSPQVPTCDVFRPSNP 659
DB 601 LIANPPTLDAMTEIHEYNQDLIRKGOANKVKLSIIVSLGTRSGRSPQVPTCDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 15
US-08-555-568B-17
; Sequence 17, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match 57.6%; Score 2084; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 2.9e-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSGVTNLFSPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
DB 1 MQFFGRLVNTFSGVTNLFSPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
QY 61 NPNRSQSGFRLFQLELEADALVNPHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNPHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECPHHSRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVILL 240
DB 181 VTDYKGETVFFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVILL 240
QY 241 LCNARCNMGNGYPIHSAMKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAMKFSQKGAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDFGETPTFLASKIG 394

Search completed: May 26, 2005, 14:21:59
Job time : 27.3333 secs


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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-2

Query Match          91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTSGVTNLFNSNPRFVKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVILV 60
DB 1 MQFFGRLVNTLSSVTNLFNSNPRFVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60

QY 61 NPNRSQSQGRFLFOLEADALVNFHOYSQQLPPFYESSQVLHTEVLOHLDLIRNHPSW 120
DB 61 SPRNPHSGFRFLFOLESEADALVNFQOFSQQLPPFYESSQVLHVEVLOHLSDLIRSHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDEIILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVLQLLGNKASAGLNQVNOGLTPLHLACQMGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKFSSQKGCACMIISMDSSQIHSDKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNVMPGSGFFPIHTAMKFSQKGCACMIISMDSSQIHSDKDPYRGASPLHWAKNAEWA 300

QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRFDVCMVLLTYGANAGTPGHEGNTPLHLAISK 360

QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNMEMIKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420

QY 420 RTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGTGLALAILHKSXM 479
DB 421 RIHDLHLLCLDGGGVKGLVLIQLLIAIEKASGVATKDLFDWVAGTSTGGTGLALAILHKSXM 480

QY 480 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLEKFEGETKMTDVRKPKVMTLGTLSDRQPA 539
DB 481 AYMRGVYFRMKDEVPFRGSRPYESGPLEBFLEKFEGETKMTDVKPKVMTLGTLSDRQPA 540

QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFFRPNRFLDGG 600

QY 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDMIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660

QY 660 WLAKTVFGAKELGKMWVDCCTDPGR 686
DB 661 WLAKTVFGAKELGKMWVDCCTDPGR 687
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RESULT 12

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US-09-519-223-2
; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-2

Query Match          91.2%; Score 3302.5; DB 3; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGRLVNTSGVTNLFNSNPRFVKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVILV 60
DB 1 MQFFGRLVNTLSSVTNLFNSNPRFVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60

QY 61 NPNRSQSQGRFLFOLEADALVNFHOYSQQLPPFYESSQVLHTEVLOHLDLIRNHPSW 120
DB 61 SPRNPHSGFRFLFOLESEADALVNFQOFSQQLPPFYESSQVLHVEVLOHLSDLIRSHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDEIILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVLQLLGNKASAGLNQVNOGLTPLHLACQMGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKFSSQKGCACMIISMDSSQIHSDKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNVMPGSGFFPIHTAMKFSQKGCACMIISMDSSQIHSDKDPYRGASPLHWAKNAEWA 300

QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRFDVCMVLLTYGANAGTPGHEGNTPLHLAISK 360

QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNMEMIKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420

QY 420 RTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGTGLALAILHKSXM 479
DB 421 RIHDLHLLCLDGGGVKGLVLIQLLIAIEKASGVATKDLFDWVAGTSTGGTGLALAILHKSXM 480

QY 480 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLEKFEGETKMTDVRKPKVMTLGTLSDRQPA 539
DB 481 AYMRGVYFRMKDEVPFRGSRPYESGPLEBFLEKFEGETKMTDVKPKVMTLGTLSDRQPA 540

QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTFFRPNRFLDGG 600

QY 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDMIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
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QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSSAGNTALHVGVMNRNRPDCVMVLLTYGANAGTPEGHNTPLHLAISK 360
QY 361 DNVEIMKALIVFCAEVDVTDNDGFTPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFCAEVDVTDNDGFTPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
DB 421 RIHDLHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFGRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMYFRMKDEVFGRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVIREPRENQNLKPPQADQLVWRAARSSGAAPTFRPNRGLDGG 599
DB 541 ELHLFRNYDAPETVIREPRENQNLKPPQADQLVWRAARSSGAAPTFRPNRGLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKMVDCCTDPDGR 687

RESULT 10

US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGLVNTFSQVTLNFSNPRVKEVAVADYTSSDRVEEGQLILFQNTPRNTWDCVLY 60
DB 1 MOFFGLVNTLSVTLNFSNPRVKEISVADYTSHERVVEEGQLILFQNASRNTWDCILV 60
QY 61 NPNRQSQGRFLFOLEADALNPNFHOYSQQLLPFYESSQVLHTEVQLHLDLIRNHPGW 120
DB 61 SPNPHSGRFLQLESEADALNPNFQSSQLPPFYESSQVLHTEVQLHLDLIRNHPGW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENBEGCTPLHLACRGDGGILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEBEGCTPLHLACRGDSSILVELVQYCHAQMD 180

QY 181 VTDYKGETVFHYAVQCDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGQEMVRVLL 240
DB 181 VTDNRGETAFHYAVQCDNSQVQLLGRNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAWKFSQKCAEMIIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300
DB 241 LCNARCNVMGSPGFPPIHTAMKFSQKCAEMIIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSSAGNTALHVGVMNRNRPDCVMVLLTYGANAGTPEGHNTPLHLAISK 360
QY 361 DNVEIMKALIVFCAEVDVTDNDGFTPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFCAEVDVTDNDGFTPTFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
DB 421 RIHDLHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFGRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMYFRMKDEVFGRSGRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVIREPRENQNLKPPQADQLVWRAARSSGAAPTFRPNRGLDGG 599
DB 541 ELHLFRNYDAPETVIREPRENQNLKPPQADQLVWRAARSSGAAPTFRPNRGLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKMVDCCTDPDGR 687

RESULT 11

US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid

Qy	546	NYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYFRPNGRFLDGGLLANNP	605
Db	614	NYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYFRPNGRFLDGGLLANNP	673
Qy	606	TLDAMTEIHEYNQDLIRKGQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWELAKT	665
Db	674	TLDAMTEIHEYNQDLIRKGQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNPWELAKT	733
Qy	666	VFGAKELGMVVDDCTDPDGR	686
Db	734	VFGAKELGMVVDDCTDPDGR	754
RESULT 8			
US-08-281-193-2			
; Sequence 2, Application US/08281193			
; Patent No. 5466595			
; GENERAL INFORMATION:			
; APPLICANT: Jones, Simon			
; APPLICANT: Tang, Jim			
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B			
; NUMBER OF SEQUENCES: 15			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/281,193			
; FILING DATE:			
; CLASSIFICATION: 435			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 752 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-281-193-2			
Query Match 91.2%; Score 3302.5; DB 1; Length 752;			
Best Local Similarity 90.4%; Pred. No. 0;			
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1			
Qy	1	MQFFGRLVNTFSGVNTLFSNPVRPRKEVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV	60
Db	1	MQFFGRLVNTLSSVNTLFSNPVRKEISVADYISHRVREEGQLILFQNASRNTWDCILV	60
Qy	61	NPRNSQSGFRFLFQLEADALVNFHQYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW	120
Db	61	SPRNPHSQGRFLFQLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW	120
Qy	121	SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDSGEIILVELVQYCHTQMD	180
Db	121	TVTHLAVELGIRECFPHHSRIISCANSTENEECTPLHLACRKGDSGEIILVELVQYCHAQMD	180
Qy	181	VTDYKGETVFHYAVOGDINSQVLLQGLGRNAVAGLNVNNOGLTPLHLACQLGQEMVRVLL	240
Db	181	VTDNKGETAHYAVAVOGDINSQVLLQGLKGNASAGLNQVNGQLTPLHLACQMGQEMVRVLL	240
Qy	241	LCNARCNTMGPNGYPIYTHAMKPSQKGCAPMIISMDSSQIHSKDPRYGASPLHWAKNAEWA	300
Db	241	LCNARCNVMGSGPFIHTAMKFSQKGCAPMIISMDSSQIHSKDPRYGASPLHWAKNAEWA	300
Qy	301	RMLLRGCNCNVNSTSSAGNTALHVGVMRNPFDCAIVLLITHGANADARGEHNTPLHLAMSK	360
Db	301	RMLLRKGCNDVSTSSAGNTALHVAVMRNPFDCAIVLLITYGANAGTFGEHNTPLHLATISK	360
Qy	361	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK	419
Db	361	DNMEMIKALIVFGAEVDTPNDFGETPAFWASKISQQLQDLMPISRARKPAFTILSSMRDEK	420
Qy	420	RTDHLHLLCDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGTILALAILHKSMS	479

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICANT: VENTER, J. Craig et al.
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 4; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQPFGRLVNTFSGVTNLFNSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQPFGRLVNTFSGVTNLFNSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTVEVQLHTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTVEVQLHTDLIRNHPWS 120
QY 121 SVAHLAVELGIRCFPHSRRIISCANCAENEECTPLHLACRKGDBGILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRCFPHSRRIISCANCAENEECTPLHLACRKGDBGILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMIKALIVFGAEVDTFNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMIKALIVFGAEVDTFNDFGETPTFLASKIGRLQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGILLIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMS 479
DB 421 RTHDHLCLDGGVKGILLIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMS 480
QY 480 AYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 539
DB 481 AYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPA 540
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DB 541 ELHLFNYDAPETVREPRNQNVNLPAPQPSQLVWRAARSGAAPTFRNGRFLDGG 600
QY 600 LLANPFLDAMTEIHYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
DB 601 LLANPFLDAMTEIHYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660

QY 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688
RESULT 7
US-09-949-016-10948
; Sequence 10948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10948
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10948
Query Match 98.5%; Score 3566.5; DB 4; Length 819;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
QY 1 MQPFGRLVNTFSGVTNLFNSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 14 MQPFGRLVNTFSGVTNLFNSNPFVRKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 73
QY 61 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTVEVQLHTDLIRNHPWS 120
DB 74 NPNRSQSGRLFOLELEADALVNFHOYSSQLLPFYESSQVLTVEVQLHTDLIRNHPWS 133
QY 121 SVAHLAVELGIRCFPHSRRIISCANCAENEECTPLHLACRKGDBGILVELVOYCHTQMD 180
DB 134 SVAHLAVELGIRCFPHSRRIISCANCAENEECTPLHLACRKGDBGILVELVOYCHTQMD 193
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 194 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 253
QY 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA 300
DB 254 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQIHSKDPRIYGASPLHWAKNAEMA 313
QY 301 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 314 RMLLKRCGNVNTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 373
QY 361 DNVEIMIKALIVFGAEVDTFNDFGETPTFLASKIGK----- 395
DB 374 DNVEIMIKALIVFGAEVDTFNDFGETPTFLASKIGRLVTRKAILTLARTVGAECYCPPIHG 433
QY 396 -----LQDLMIHSRARKPAFILGSMRDEKRTDHL 425
DB 434 VPAEQSSAAPHHPFSLERAQPPFI SLNNLEQLQDLMIHSRARKPAFILGSMRDEKRTDHL 493
QY 426 LCLDGGVKGILLIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMSMYMRGM 485
DB 494 LCLDGGVKGILLIQLLIAIEKASGVATKDLFDWAGTSTGGILALAILHKSMSMYMRGM 553
QY 486 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 545
DB 554 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTGTLSDRQPAELHLFR 613

QY 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
QY 301 RMLLKRCNCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCNCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKM 479
DB 421 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKM 480
QY 480 AYMRGMVFRMKDEVRFRSGRPSYSGPLEEFLEKFEHGTMTDVRKPKVMTLTGTLSDRQPA 539
DB 481 AYMRGMVFRMKDEVRFRSGRPSYSGPLEEFLEKFEHGTMTDVRKPKVMTLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIIVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIIVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMVVDCCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688

RESULT 5

US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-519-223-23

Query Match 99.6%; Score 3606.5; DB 3; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
DB 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
QY 61 NPNRSQSQRFLFOLEADALVNFHOYSQQLLPFYESSQVLTVEVLQHLTLIRNHPSW 120
DB 61 NPNRSQSQRFLFOLEADALVNFHOYSQQLLPFYESSQVLTVEVLQHLTLIRNHPSW 120
QY 121 SVAHLAVELGIRECFPHSRIRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHSRIRIISCANCAENEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSOVLQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSOVLQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
DB 241 LCNARCNMGNGYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYKASPLHAKNAEMA 300
QY 301 RMLLKRCNCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCNCVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKM 479
DB 421 RTHDHLCLDGGVKGKLIIOILLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKM 480
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DB 481 AYMRGMVFRMKDEVRFRSGRPSYSGPLEEFLEKFEHGTMTDVRKPKVMTLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIIVSLGTGRSPQVPVTCVDVFRPSNP 659
DB 601 LLANNPTLDAMTEIHEYNDLIRKQANKVKLSIIVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMVVDCCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMVVDCCCTDPDGRP 688

RESULT 6

US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;
;
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 3620; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
Db 61 NPNRSQSGFRLFQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
QY 121 SVAHLAVALGIRECFPHSRIRISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
Db 121 SVAHLAVALGIRECFPHSRIRISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVPHYAVQGDNSQVLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCINMGPNYPIHSAKMFQKGAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPNYPIHSAKMFQKGAEMIIISMDSSQIHSDKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCNVNNTSSAGNTALHVGVMNRPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCNVNNTSSAGNTALHVGVMNRPFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVMETKALVFGAEVDTFNDGETPTFLASKTGKLDLMHISRARKPAPILGSMDEKR 420
Db 361 DNVMETKALVFGAEVDTFNDGETPTFLASKTGKLDLMHISRARKPAPILGSMDEKR 420
QY 421 THDHLCLDGGVKGKLIILQLLTAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480
Db 421 THDHLCLDGGVKGKLIILQLLTAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMA 480
QY 481 YMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAE 540
Db 481 YMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAE 540

;
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: US/08/555,568B
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-23

Query Match 99.6%; Score 3606.5; DB 2; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
Db 61 NPNRSQSGFRLFQLELEADALVNFHOYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
QY 121 SVAHLAVALGIRECFPHSRIRISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
Db 121 SVAHLAVALGIRECFPHSRIRISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVPHYAVQGDNSQVLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMVRVLL 240
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121 SVHHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIIVELVQYCHTQMD 180
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181 VTDYKGETVFHYAVOGDINSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240
181 VTDYKGETVFHYAVOGDINSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240
241 LCNARCNIMGNGPYPIHSAKFSGKCAEMIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
241 LCNARCNIMGNGPYPIHSAKFSGKCAEMIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
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301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALAILHKSNA 480
421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALAILHKSNA 480
481 YMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDROPAP 540
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601 LANNPTLDAMTEIHEYNOQLIRKGQANKVKLSIIVVSLGTGRSPQVPTVCDVFRPSNPW 660
601 LANNPTLDAMTEIHEYNOQLIRKGQANKVKLSIIVVSLGTGRSPQVPTVCDVFRPSNPW 660
661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687
661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 2

US-09-519-223-21
; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-21

Query Match 100.0%; Score 3620; DB 3; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MQFFGLVNTSGVTNLFSPFRVKEVAVADYTSDDRVRREGQLLFFONTNRTWDCVLV 60
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DB 61 NPNRSQSGFRLLFOLELEADALVNFHQYSSQLLPFYESSPOVLHTEVLOHLDLIRNHPSW 120
QY 121 SVHHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIIVELVQYCHTQMD 180
DB 121 SVHHLAVELGIRECFHHSRIISCANCAENEBECTPLHLACRKGDEIIVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGQKQEMVRVLL 240
QY 241 LCNARCNIMGNGPYPIHSAKFSGKCAEMIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNIMGNGPYPIHSAKFSGKCAEMIISMDSSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGKQLQDLMIHSRARKPAFIIIGSMRDEKR 420
QY 421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALAILHKSNA 480
DB 421 THDHLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGIILALAILHKSNA 480
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DB 481 YMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTGTLSDROPAP 540
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DB 541 LHLFRNYDAPETVREPRFNQVNLPPAQPDSQVRAARSSGAAPTFRPNRFLDGL 600
QY 601 LANNPTLDAMTEIHEYNOQLIRKGQANKVKLSIIVVSLGTGRSPQVPTVCDVFRPSNPW 660
DB 601 LANNPTLDAMTEIHEYNOQLIRKGQANKVKLSIIVVSLGTGRSPQVPTVCDVFRPSNPW 660
QY 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 ELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 3

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 25.3333 Seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MOFFGRLVNTFSGVNLFNSN.....GAKELGKVVVDCTPDGGRP 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
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1	3620	100.0	687	2	US-08-555-568B-21	Sequence 21, Appl
2	3620	100.0	687	3	US-09-519-223-21	Sequence 21, Appl
3	3620	100.0	687	4	US-09-927-180-21	Sequence 21, Appl
4	3606.5	99.6	688	2	US-08-555-568B-23	Sequence 23, Appl
5	3606.5	99.6	688	3	US-09-519-223-23	Sequence 23, Appl
6	3606.5	99.6	688	4	US-09-927-180-23	Sequence 23, Appl
7	3566.5	98.5	819	4	US-09-949-016-10948	Sequence 10948, A
8	3302.5	91.2	752	1	US-08-281-193-2	Sequence 2, Appli
9	3302.5	91.2	752	1	US-08-422-106-2	Sequence 2, Appli
10	3302.5	91.2	752	2	US-08-735-716-2	Sequence 2, Appli
11	3302.5	91.2	752	2	US-08-555-568B-2	Sequence 2, Appli
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14	3302.5	91.2	752	5	PCT-US95-08069-2	Sequence 2, Appli
15	2084	57.6	394	2	US-08-555-568B-17	Sequence 17, Appl
16	2084	57.6	394	3	US-09-519-223-17	Sequence 17, Appl
17	2084	57.6	394	4	US-09-927-180-17	Sequence 17, Appl
18	1531	42.3	292	2	US-08-555-568B-19	Sequence 19, Appl
19	1531	42.3	292	3	US-09-519-223-19	Sequence 19, Appl
20	1531	42.3	292	4	US-09-927-180-19	Sequence 19, Appl
21	1163.5	32.1	896	4	US-09-270-767-46130	Sequence 46130, A
22	902.5	24.9	545	4	US-09-270-767-61684	Sequence 61684, A
23	371	10.2	143	4	US-09-270-767-33298	Sequence 33298, A
24	338	9.3	843	2	US-09-172-977-3	Sequence 3, Appli
25	338	9.3	843	4	US-09-404-108-3	Sequence 4, Appli
26	332	9.2	1839	2	US-09-172-977-4	Sequence 4, Appli
27	332	9.2	1839	4	US-09-404-108-4	Sequence 4, Appli

28	332	9.2	2753	4	US-09-949-016-7659	Sequence 7659, Ap
29	332	9.2	2753	4	US-09-949-016-7660	Sequence 7660, Ap
30	332	9.2	3924	4	US-09-538-092-1246	Sequence 1246, Ap
31	305.5	8.4	1745	2	US-09-031-485-33	Sequence 33, Appl
32	305.5	8.4	1745	2	US-08-847-429A-33	Sequence 33, Appl
33	305.5	8.4	1745	3	US-09-065-474-33	Sequence 33, Appl
34	305.5	8.4	1745	3	US-09-557-034-33	Sequence 33, Appl
35	302	8.3	786	4	US-09-509-802-2	Sequence 2, Appli
36	302	8.3	787	3	US-09-188-930-334	Sequence 334, App
37	302	8.3	787	4	US-09-312-283C-334	Sequence 2, Appli
38	286	8.2	1088	3	US-09-082-059-2	Sequence 334, App
39	296	8.2	3913	4	US-09-949-016-10933	Sequence 10933, A
40	296	8.2	4377	4	US-09-949-016-6978	Sequence 6978, Ap
41	294	8.1	1719	4	US-09-949-016-6966	Sequence 6966, Ap
42	294	8.1	1856	4	US-09-949-016-6964	Sequence 6964, Ap
43	294	8.1	1880	4	US-09-949-016-5876	Sequence 5876, Ap
44	294	8.1	1881	4	US-09-949-016-6965	Sequence 6965, Ap
45	294	8.1	1883	4	US-09-949-016-9010	Sequence 9010, Ap

ALIGNMENTS

RESULT 1
US-08-555-568B-21
; Sequence 21, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-21

Query Match		100.0%;	Score 3620;	DB 2;	Length 687;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 687;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MOFFGRLVNTFSGVNLFNSNPFVRKEVAVADYTS	SDRVEEGQLILFQNTPNRTWDCVLV	60	
DB	1	MOFFGRLVNTFSGVNLFNSNPFVRKEVAVADYTS	SDRVEEGQLILFQNTPNRTWDCVLV	60	
QY	61	NPRNSQSGRLPQLELEADALVNFHQYSSQLLPFF	YESSQVLHTEVQLHQLTDLIRNHPSW	120	
DB	61	NPRNSQSGRLPQLELEADALVNFHQYSSQLLPFF	YESSQVLHTEVQLHQLTDLIRNHPSW	120	

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Job time : 95.6667 secs

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PT	infections.	
PS	Claim 69; Page 206-207; 238pp; English.	
XX		
CC	The present sequence is the protein sequence of human lipid-associated	
CC	molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows	
CC	homology to human Ca2+-independent phospholipase A2 short isoform. This	
CC	is one of 19 LIPAM polypeptides of the invention. The invention relates	
CC	to these novel LIPAMs and the nucleic acids encoding them, and to the use	
CC	of nucleic acids and proteins in the diagnosis, treatment and prevention	
CC	of disorders associated with abnormal expression or activity of LIPAM	
CC	such as neurodegenerative disorders (e.g. Parkinson's disease,	
CC	Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,	
CC	catatonja), endocrine disorders (e.g. diabetes, Grave's disease), cancers	
CC	(e.g. leukemia, cervical or breast cancers), immunological disorders	
CC	(e.g. scleroderma, systemic lupus erythematosus, allergies),	
CC	gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.	
CC	Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,	
CC	parasitic, protozoal, helminthic), cardiovascular disorders (e.g.	
CC	atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention	
CC	also relates to the assessment of the effects of exogenous compounds on	
CC	the expression of nucleic acids and LIPAMs. The invention provides	
CC	expression vectors, host cells, antibodies, agonists and antagonists,	
CC	transgenic organisms, and arrays and microarrays of the polynucleotides.	
XX		
SQ	Sequence 784 AA;	
Query Match 99.3%; Score 3593.5; DB 7; Length 784;		
Best Local Similarity 99.6%; Pred. No. 0;		
Matches 684; Conservative 1; Mismatches 1; Indels 1; Gaps 1;		
QY	1 MOFFGRLVNTFSGVNTLFSNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
DB	33 MOFFGRLVNTFSGVNTLFSNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 92	
QY	61 NPNRSQSGRLFQLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPSW 120	
DB	93 NPNRSQSGRLFQLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPSW 152	
QY	121 SVAHLAVALGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDGGEILVELVQYCHTQMD 180	
DB	153 SVAHLAVALGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDGGEILVELVQYCHTQMD 212	
QY	181 VTDYKGETVFHVAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240	
DB	213 VTDYKGETVFHVAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 272	
QY	241 LCNARCNIMGNGYPITHSANKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAWA 300	
DB	273 LCNARCNIMGNGYPITHSANKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAWA 332	
QY	301 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360	
DB	333 RMLLKRGCVNNTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 392	
QY	361 DNVEIMKALIVFGAEVDTNDPGETFTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 419	
DB	393 DNVEIMKALIVFGAEVDTNDPGETFTFLASKIGK-LQDLMIHSRARKPAFILGSRDEK 452	
QY	420 RTHDHLCLDGGVKGILLIIOILLIALEKASGVATKDLFDWAGTSGGILAILHLSKSM 479	
DB	453 RTHDHLCLDGGVKGILLIIOILLIALEKASGVATKDLFDWAGTSGGILAILHLSKSM 512	
QY	480 AYMRGMYFRMKQEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMLTGTLSDRQA 539	
DB	513 AYMRGMYFRMKQEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMLTGTLSDRQA 572	
QY	540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGG 599	
DB	573 ELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGG 632	
QY	600 LLANNPTLDAMTEIHYNQDLIRKGQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 692	

DB	633 LLANNPTLDAMTEIHYNQDLIRKGQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 692	
QY	660 WELAKTVFGAKELGKMWVDCCTDPDGR 686	
DB	693 WELAKTVFGAKELGKMWVDCCTDPDGR 719	
RESULT 6		
AAE25968		
ID	AAE25968 standard; protein; 806 AA.	
XX		
AC	AAE25968;	
XX		
DT	15-NOV-2002 (first entry)	
XX		
DE	Human PLA2 group VI (Ca2+-independent) protein.	
XX		
KW	Human; antisense; phospholipase A2; infection; inflammation; tumour;	
KW	antisense therapy; PLA2 protein.	
XX		
OS	Homo sapiens.	
XX		
PN	US6410325-B1.	
XX		
PD	25-JUN-2002.	
XX		
PF	09-MAY-2001; 2001US-00851896.	
XX		
PR	09-MAY-2001; 2001US-00851896.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett CF, Freier SM, Watt AT;	
XX		
DR	WPI; 2002-616513/66.	
DR	N-PSDB; AAD42941.	
XX		
PT	Novel antisense compounds useful for inhibiting gene expression of human	
PT	phospholipase A2, group VI and for treating diseases associated with	
PT	expression of phospholipase A2, group VI.	
XX		
PS	Disclosure; Col 109-116; 72pp; English.	
XX		
CC	The present invention relates to novel antisense compounds which inhibit	
CC	the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).	
CC	The invention is useful for inhibiting the expression of PLA2, group VI	
CC	(Ca2+-independent) in human cells or tissues and for treating an animal,	
CC	particularly a human suspected of having or being prone to a disease or	
CC	condition associated with expression of human PLA2, group VI (Ca2+-	
CC	independent). It is useful for diagnostics, therapeutics and as research	
CC	reagent, e.g. prophylactically to prevent or delay infection, tumour	
CC	formation or inflammation. The present sequence is human PLA2 group VI	
CC	(Ca2+-independent) protein	
XX		
SQ	Sequence 806 AA;	
Query Match 98.5%; Score 3566.5; DB 5; Length 806;		
Best Local Similarity 92.3%; Pred. No. 0;		
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;		
QY	1 MOFFGRLVNTFSGVNTLFSNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
DB	1 MOFFGRLVNTFSGVNTLFSNPRFVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
QY	61 NPNRSQSGRLFQLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPSW 120	
DB	61 NPNRSQSGRLFQLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHQLTDLIRNHPSW 120	
QY	121 SVAHLAVALGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDGGEILVELVQYCHTQMD 180	
DB	121 SVAHLAVALGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDGGEILVELVQYCHTQMD 180	
QY	181 VTDYKGETVFHVAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240	

Db 181 VTDYKGETVFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTFLHLACQLGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCGNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMIKALIVFGAEVDPNDFGETPTFLASKIGK-----LQDLMHISRARKPAFILGSMRDEKTHDL 395
Db 361 DNVEIMIKALIVFGAEVDPNDFGETPTFLASKIGRLVTRKAILTLRLTVGABYCFFPIHG 420
QY 396 -----LQDLMHISRARKPAFILGSMRDEKTHDL 425
Db 421 VPAEQGSAAHPHPSLERAQPPISLNNLELQDLMHISRARKPAFILGSMRDEKTHDL 480
QY 426 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 485
Db 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 540
QY 486 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 545
Db 541 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 600
QY 546 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 605
Db 601 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 660
QY 606 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAKT 665
Db 661 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAKT 720
QY 666 VFGAKELGMVVDCCDDPDGR 686
Db 721 VFGAKELGMVVDCCDDPDGR 741
RESULT 7
ADO19776
ID ADO19776 standard; protein; 806 AA.
AC ADO19776;
XX
DT 12-AUG-2004 (first entry)
DE Human PRO polypeptide #350.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;

XX WPI; 2004-420067/39.
DR N-PSDB; ADO19775.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX
PS Claim 7; SEQ ID NO 700; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 806 AA;
Query Match 98.5%; Score 3566.5; DB 8; Length 806;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
QY 1 MQFFGLRVNTSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLRVNTSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLLPFYESSPQVLHTEVLQHLTDLIRNHP 120
Db 61 NPNRSQSGFRLFQLELEADALVNFHOYSQQLLPFYESSPQVLHTEVLQHLTDLIRNHP 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTFLHLACQLGQEMVRVLL 240
Db 181 VTDYKGETVFHYAVOGDNSQVQLLGRNAVAGLNVNNOGLTFLHLACQLGQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPIHSAKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCGNVNSTSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMIKALIVFGAEVDPNDFGETPTFLASKIGK-----LQDLMHISRARKPAFILGSMRDEKTHDL 395
Db 361 DNVEIMIKALIVFGAEVDPNDFGETPTFLASKIGRLVTRKAILTLRLTVGABYCFFPIHG 420
QY 396 -----LQDLMHISRARKPAFILGSMRDEKTHDL 425
Db 421 VPAEQGSAAHPHPSLERAQPPISLNNLELQDLMHISRARKPAFILGSMRDEKTHDL 480
QY 426 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 485
Db 481 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 540
QY 486 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 545
Db 541 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 600
QY 546 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 605
Db 601 NYDAPETVREPRFNQNVNLRPPAQSDQLVRAARSSGAAPTYPFRPNRFLDGGLLANNP 660

QY 606 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAKT 665
 Db 661 TLDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWELAKT 720
 QY 666 VFGAKELGKMWVDDCCTDPDGR 686
 Db 721 VFGAKELGKMWVDDCCTDPDGR 741

RESULT 8
 ABM84355
 ID ABM84355 standard; protein; 810 AA.
 AC ABM84355;
 DT 18-NOV-2004 (first entry)
 XX Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX Homo sapiens.
 XX WO2004023973-A2.
 PN 25-MAR-2004.
 PD 12-SEP-2003; 2003WO-US028227.
 PF 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panear IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JM, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patursky S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN43007.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX Claim 27; Page; 190pp; English.
 PS The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX Sequence 810 AA;

Query Match 97.9%; Score 3544.5; DB 8; Length 810;
 Best Local Similarity 91.8%; Pred. No. 0;
 Matches 684; Conservative 1; Mismatches 1; Indels 59; Gaps 3;
 QY 1 MOFFGRLVNTFSQVNTLFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 Db 1 MOFFGRLVNTFSQVNTLFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
 QY 61 NPRNSQSGFRLFQLELEADALVNFHOYSQQLLPFFYESSQVLTHTVQLHTLDIRNHPSW 120
 Db 61 NPRNSQSGFRLFQLELEADALVNFHOYSQQLLPFFYESSQVLTHTVQLHTLDIRNHPSW 120
 QY 121 SVAHLAVALGIRECFHHSRII-----SCANCANEEG 152
 Db 121 SVAHLAVALGIRECFHHSRIIIRVSAHQVPGWLWELISTHEIEFFSPPXSCANCANEEG 180
 QY 153 CTPLHLACRKGDEILVELVQYCHTQMDVTFHYAVQGDNSQVLQLGRNAVAG 212
 Db 181 CTPLHLACRKGDEILVELVQYCHTQMDVTFHYAVQGDNSQVLQLGRNAVAG 240
 QY 213 LNOVNNQGLTPLHLACQLGKQEMVRVLLCNARCINMGPNGYPIHSAMKFSQKGCAMII 272
 Db 241 LNOVNNQGLTPLHLACQLGKQEMVRVLLCNARCINMGPNGYPIHSAMKFSQKGCAMII 300
 QY 273 SMDSSQIHSKDPYRGASPLHWAQNAEMARMLKRCNCVNSTSSAGNTALHVGVMRNFDC 332
 Db 301 SMDSSQIHSKDPYRGASPLHWAQNAEMARMLKRCNCVNSTSSAGNTALHVGVMRNFDC 360
 QY 333 AIIVLLTHGANADARGEHNTPLHLAMS KDNVEMI KALIVFGAEVDTPNDFGETPTFLASK 392
 Db 361 AIIVLLTHGANADARGEHNTPLHLAMS KDNVEMI KALIVFGAEVDTPNDFGETPTFLASK 420
 QY 393 IGK-LQDLMLHISRAKPAFIFLGSMDRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGV 451
 Db 421 IGKQLQDLMLHISRAKPAFIFLGSMDRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGV 480
 QY 452 ATKOLFDMVAGTSTGGILALAILHKSMAVMYMRMDEVPFRSGRPYSGPSEFLFKR 511
 Db 481 ATKOLFDMVAGTSTGGILALAILHKSMAVMYMRMDEVPFRSGRPYSGPSEFLFKR 540
 QY 512 EFGHTKMTDVRKPK-----VMLTGTLSDRQPAEL 541
 Db 541 EFGHTKMTDVRKPKLDQSDTPPALPERACFAGVMRGEAHLSETEVMLTGTLSDRQPAEL 600
 QY 542 HLFNRYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGLL 601
 Db 601 HLFNRYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGLL 660
 QY 602 ANNPILDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWE 661
 Db 661 ANNPILDAMTEIHEYNDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNPWE 720
 QY 662 LAKTVFGAKELGKMWVDDCCTDPDGR 686
 Db 721 LAKTVFGAKELGKMWVDDCCTDPDGR 745

RESULT 9
 ABM84354
 ID ABM84354 standard; protein; 810 AA.
 AC ABM84354;
 XX 18-NOV-2004 (first entry)
 DT Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
 DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX Homo sapiens.
 XX WO2004023973-A2.
 PN 25-MAR-2004.
 PD 12-SEP-2003; 2003WO-US028227.
 PF 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panear IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JM, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patursky S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN43007.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX Claim 27; Page; 190pp; English.
 PS The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX Sequence 810 AA;

CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
CC and other disease mediated by increased levels of prostaglandins,
CC leukotriene or platelet activating factor. The enzyme can also be used
XX for the production of antibodies for use as research or diagnostic tools
SQ Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCILV 60
QY 61 NPNRSOGFRLFQLEADALVNFHQSOLLFPYESSQVLTHTVQLHQLTDLIRNHPWS 120
Db 61 SPRNPHSGFRLFQLESEADALVNFQFSSQLPFYESSQVLTHTVQLHQLTDLIRSHPSW 120
QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDSBILVELVQYCHTQMD 180
Db 121 TVTHLAVALGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSBILVELVQYCHQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLTGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGETAFHYAVQGDNSQVLTGLGRNAVAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIMGPNCGYPIHSAKMSQKCAEMIISMDSQHSQIPRYCASPLHWAKNAEMA 300
Db 241 LCNARCNVMPGSPGFPHTAMKFSQKCAEMIISMDSQHSQIPRYCASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCVDVSTSAAGNTALHVVAVNRNFDCAIVLLTHGANAGTPEHGTPLHLAISK 360
QY 361 DNWEMIKALIVFGAEVDTNDFTETFLASKIGK-LQDLMHISRARKPAFILGSRMRDEK 419
Db 361 DNWEMIKALIVFGAEVDTNDFTETPAFASKISKQLQDLMPISRARKPAFILSSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKOLFDMVAGTSTGGILAILHLSKSM 479
Db 421 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKOLFDMVAGTSTGGILAILHLSKSM 480
QY 480 AYMRGMYFMKQDVFRGSPYEGSPLLEFLKRFEGEHTKMTDVRKPKVMLTGTLSRQPA 539
Db 481 AYMRGYFMKQDVFRGSPYEGSPLLEFLKRFEGEHTKMTDVRKPKVMLTGTLSRQPA 540
QY 540 ELHLFRNYDAPETVREPRNQNLPPAPQPSQVLRARSSGAAPTFRPNRGLDGG 599
Db 541 ELHLFRNYDAPETVREPRNQNLPPAPQPSQVLRARSSGAAPTFRPNRGLDGG 600
QY 600 LLANNPTLDAMTEIHEYNODLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNODMIRKQGNKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 11
ID AA001479
XX AA001479 standard; protein; 752 AA.
AC AA001479;
XX
XX
DT 25-MAR-2003 (revised)
DT 12-FEB-1997 (first entry)
DE
DE
XX Calcium-independent cytosolic phospholipase A2/B.
XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonoyl-phosphatidylcholine;

KW anti-inflammatory; screen; rheumatoid arthritis.
OS Synthetic.
XX US5554511-A.
XX 10-SEP-1996.
XX 14-APR-1995; 95US-00422420.
XX 27-JUL-1994; 94US-00281193.
XX (GEMY) GENETICS INST INC.
XX Tang J, Jones S;
XX WPI; 1996-424653/42.
XX N-PSDB; AAT44578.
XX Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing host cells contg. the phospholipase gene, useful for screening anti-inflammatory agents for treating e.g. rheumatoid arthritis.
XX Claim 1; Col 15-22; 24pp; English.
XX The present sequence is that of a calcium-independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release of arachidonic acid in specific tissues characterised by unique membrane phospholipids. The invention provides a process for producing such an enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence of one or more amino acid sequences selected from AA001480-92; cPLA2/B has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-arachidonoyl-phosphatidylcholine. The enzyme is useful for screening anti-inflammatory agents mediated by the arachidonic acid cascade, for treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLVNTFSVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGLVNTLSSVTNLFNSNPFVKVAVADYTSDDRVREEGQLILFQNTPNRTWDCILV 60
QY 61 NPNRSOGFRLFQLEADALVNFHQSOLLFPYESSQVLTHTVQLHQLTDLIRNHPWS 120
Db 61 SPRNPHSGFRLFQLESEADALVNFQFSSQLPFYESSQVLTHTVQLHQLTDLIRSHPSW 120
QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEBCGCTPLHLACRKGDSBILVELVQYCHTQMD 180
Db 121 TVTHLAVALGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSBILVELVQYCHQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLTGLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGETAFHYAVQGDNSQVLTGLGRNAVAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIMGPNCGYPIHSAKMSQKCAEMIISMDSQHSQIPRYCASPLHWAKNAEMA 300
Db 241 LCNARCNVMPGSPGFPHTAMKFSQKCAEMIISMDSQHSQIPRYCASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCVDVSTSAAGNTALHVVAVNRNFDCAIVLLTHGANAGTPEHGTPLHLAISK 360
QY 361 DNWEMIKALIVFGAEVDTNDFTETFLASKIGK-LQDLMHISRARKPAFILGSRMRDEK 419
Db 361 DNWEMIKALIVFGAEVDTNDFTETPAFASKISKQLQDLMPISRARKPAFILSSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKOLFDMVAGTSTGGILAILHLSKSM 479

Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKFEHGTMTDVRKPKVMTGTLSDRQPA 539
 Db 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKFEHGTMTDVRKPKVMTGTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 599
 Db 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDDCCTDPDGR 686
 Db 661 WELAKTVFGAKELGKMWVDDCCTDPDGR 687

RESULT 12
 AAW13163
 ID AAW13163 standard; protein; 752 AA.
 XX
 AC AAW13163;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-MAY-1997 (first entry)
 XX
 DE Ca-independent phospholipase A2/B protein.
 XX
 KW Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
 KW chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
 KW heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
 KW CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.
 XX
 OS Cricetulus griseus; ovary cells.
 PN US5589170-A.
 XX
 PD 31-DEC-1996.
 PF 14-APR-1995; 95US-00422106.
 XX
 PR 27-JUL-1994; 94US-00281193.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Tang J, Jones S;
 XX
 DR WPI: 1997-076789/07.
 DR N-PSDB; AAT59199.
 XX
 PT Compens. comprising calcium-independent phospholipase enzyme - for
 PT screening for anti-inflammatory agents.
 XX
 PS Claim 5; Col 15-22; 24pp; English.
 XX
 CC This is the amino acid sequence of the Ca-independent phospholipase A2/B
 CC from Chinese hamster ovary cells. The protein was isolated from these
 CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
 CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
 CC chromatofocusing chromatography. The purified protein has mol. wt. of 86
 CC kD and an optimum pH 6. The protein was used for amino acid sequencing
 CC from which pools of degenerate probes were synthesised. The probes were
 CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 40000
 CC recombinant phages screened, 12 positive plaques were isolated. One of
 CC these, designated clone 9, contained this sequence. The phospholipase
 CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
 CC cells. The protein, or peptides derived from it e.g. AAW13164-76, can be
 CC used to identify phospholipase inhibitors that can be used as anti-
 CC inflammatory agents, esp. against components of the arachidonic acid
 CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT

CC -2003 to standardise OS field)
 XX
 SQ Sequence 752 AA;
 Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADVTSDDRVREEGQLILFQNTNRTWDCVILV 60
 Db 1 MQFFGRLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
 QY 61 NPNRSQSQGRFLFQLEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTLIRNHPSW 120
 Db 61 SPRNPHSGRFLFQLESEADALVNFQFSSQLPPFYESSVQVLHVEVQLHLSDLIRSHPSW 120
 QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDSIILVELVOYCHTQMD 180
 Db 121 TVTHLAVELGIRECFPHHSRIISCANSTENEECTPLHLACRKGDSIILVELVOYCHAQMD 180
 QY 181 VTDYKGETVHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEWVRVLL 240
 Db 181 VTDNKGETAHYAVQGDNSQVQLLLGKNASAGLNVNNOGLTPLHLACOMGQEWVRVLL 240
 QY 241 LCNARCNIMGPNGYPIHSAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 Db 241 LCNARCNVMGPGFPPIHTAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLLRGCVNVSSTAGNTALHVGVMNRFDCAIIVLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLRGCDVDSTSAAGNTALHVAVMNRFDCAIIVLTHGANADARGEHNTPLHLAISK 360
 QY 361 DNEMIKALIIVFGAEVDPNDGFTPLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
 Db 361 DNEMIKALIIVFGAEVDPNDGFTPLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420
 QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
 Db 421 RIHDLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKFEHGTMTDVRKPKVMTGTLSDRQPA 539
 Db 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKFEHGTMTDVRKPKVMTGTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 599
 Db 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFFRNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 601 LLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDDCCTDPDGR 686
 Db 661 WELAKTVFGAKELGKMWVDDCCTDPDGR 687

RESULT 13
 AAW17849
 ID AAW17849 standard; protein; 752 AA.
 XX
 AC AAW17849;
 DT 27-AUG-2003 (revised)
 DT 07-AUG-1997 (first entry)
 DE Hamster cytosolic phospholipase A2/B.
 KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KW inflammation; inhibitor; antiinflammatory; CHO.
 XX
 OS Cricetus.
 XX

FT	Key	Location/Qualifiers	
FT	Active-site	465	
FT		/notes: "mutagenesis of Ser-465 results in loss of activity"	
XX	XX	WO9717448-A2.	
XX	XX	15-MAY-1997.	
PD	XX	07-NOV-1996; 96WO-US017794.	
XX	XX	08-NOV-1995; 95US-00555568.	
PR	XX	(GEMY) GENETICS INST INC.	
XX	XX	Jones S, Tang J;	
PI	XX	WPI; 1997-281037/25.	
DR	XX	N-PSDB; AAT68827.	
DR	XX	Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.	
XX	XX	Example 4; Page 33-36; 74pp; English.	
XX	XX	A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AAT68827) obt'd. from a CHO-DUX cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.)	
XX	XX	Sequence 752 AA;	
SQ			
	Query Match	91.2%; Score 3302.5; DB 2; Length 752;	
	Best Local Similarity	90.4%; Pred. No. 0;	
	Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;		
QY	1	MOFFGRLVNTFGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60	
DB	1	MOFFGRLVNTLSSVNTLFSNPRFVKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60	
QY	61	NPRNSQSGRLFLQLEADALVNFHYQSQQLPFYESSQVLTHTVQLHQLTDLIRNHPSW 120	
DB	61	SPRNPHSGRLFLQLESEADALVNFQFSQQLPFYESSQVLTHTVQLHQLSOLIRSHPSW 120	
QY	121	SVANLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDSGLVLYVQYCHTQMD 180	
DB	121	TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSGLVLYVQYCHAQMD 180	
QY	181	VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240	
DB	181	VTDNKGETAHYAVQGDNSQVLQLGRNASAGLNQVNNQGLTPLHLACOMGQEMVRVLL 240	
QY	241	LCNARCINMGPNGYPIHSAKMSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300	
DB	241	LCNARCINMGPNGPSFPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300	
QY	301	RMLLKRCGNVNSTSAGNTALHVGVMNRNPDCAIVLLTHGANADARGEHNTPLHLAMSK 360	
DB	301	RMLLKRCGCDVSTSAAGNTALHVVAVNRNFDCAIVLLTYGANAGTPEGHNTPLHLAISK 360	
QY	361	DNVEMIKALIVFCAEVDYTDNDTFCETTELASKIGK-LQDLMIHSRARKPAFILSSMRDEK 419	
DB	361	DNVEMIKALIVFAEVDYTDNDTFCETTELASKIGK-LQDLMIHSRARKPAFILSSMRDEK 420	
QY	420	RTDHLCLLDGGGKGLIIQLLIAIEKASGVATKDLFDVAGTSTGGILAILHLSKSM 479	
DB	421	RIHDLCLLDGGGKGLVIIQLLIAIEKASGVATKDLFDVAGTSTGGILAILHLSKSM 480	
QY	480	AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGHEHTKMTDVRKPKVMTGLTSLDRQPA 539	
DB	481	AYMRGYFRMKDEVFRGSRPYESGPLEEFLEKREFGHEHTKMTDVRKPKVMTGLTSLDRQPA 540	
QY	540	ELHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPNRGFLDGG 599	
DB	541	ELHLFRNYDAPEVIREPRFNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPNRGFLDGG 600	
QY	600	LIANNPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 659	
DB	601	LIANNPTLDAMTEIHEYNQDMIRKGGNKVKLSIVVSLGTGRSPQVPTCVDFRPSNP 660	
QY	660	WELAKTVFGAKELGKMWVDCCTDPDGR 686	
DB	661	WELAKTVFGAKELGKMWVDCCTDPDGR 687	
	RESULT 14		
	AAW81825		
ID	AAW81825	standard; protein; 752 AA.	
XX	XX	AAW81825;	
AC	AAW81825;		
DT	02-FEB-1999	(first entry)	
XX	XX	Chinese hamster calcium independent cPLA2/B protein.	
DE	XX	Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening;	
XX	XX	anti-inflammatory; arachidonic acid cascade; chinese hamster.	
KW	XX	Cricetulus griseus.	
OS	XX	US5840511-A.	
PN	XX	24-NOV-1998.	
XX	XX	23-OCT-1996; 96US-00735716.	
PF	XX	27-JUL-1994; 94US-00281193.	
PR	XX	14-APR-1995; 95US-00422106.	
XX	XX	(GEMY) GENETICS INST INC.	
PA	XX	Tang J, Jones S;	
PI	XX	WPI; 1999-034032/03.	
DR	XX	N-PSDB; AAV64840.	
XX	XX	Screening assay for phospholipase inhibitors - using specified phospholipase polypeptide.	
PT	XX	Claim 1b; Col 21-24; 24pp; English.	
PS	XX	This sequence represents a novel calcium independent cytosolic phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This protein can be used for screening unknown compounds for anti-inflammatory activity mediated by the arachidonic acid cascade	
XX	XX	Sequence 752 AA;	
SQ			
	Query Match	91.2%; Score 3302.5; DB 2; Length 752;	
	Best Local Similarity	90.4%; Pred. No. 0;	
	Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;		
QY	1	MOFFGRLVNTFGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60	
DB	1	MOFFGRLVNTLSSVNTLFSNPRFVKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60	
QY	61	NPRNSQSGRLFLQLEADALVNFHYQSQQLPFYESSQVLTHTVQLHQLTDLIRNHPSW 120	
DB	61	SPRNPHSGRLFLQLESEADALVNFQFSQQLPFYESSQVLTHTVQLHQLSOLIRSHPSW 120	
QY	121	SVANLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDSGLVLYVQYCHTQMD 180	

Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACOLGQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLQVNNQGLTPLHLACOMGQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHSAKFESQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVWGSPGFPIHTAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCNCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCGCDVSDSTAAGNTALHVAVMNRFDCAIVLLTYGANAGTPEHNTPLHLAISK 360
QY 361 DNEMIKALIVFGAEVDTPEHNTPLHLAISKIGK-LQDLMIHISRAKPAFTILGSMRDEK 419
Db 361 DNEMIKALIVFGAEVDTPEHNTPLHLAISKIGK-LQDLMIHISRAKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGGVKGLIIQLLIIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
Db 421 RIHDLHLCLDGGGVKGLVIIQLLIIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFLKREFEHTKMTDVRKPKVMTLGTLSDRQPA 539
Db 481 AYMRGVYFRMKDEVPFRGSRPYESGPLEEFLKREFEHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQVNLPPAQPDSQDLVWRAARSSGAAPTFRPNRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQVNLPPAQPDSQDLVWRAARSSGAAPTFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSPN 659
Db 601 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSPN 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPGR 687

RESULT 15
ABB82215
ID ABB82215 standard; protein; 752 AA.
AC ABB82215;
XX
XX
DT 08-JAN-2003 (first entry)
XX
XX
DE Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).
XX
XX
KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
KW antiasthmatic.
XX
OS Unidentified.
XX
XX
PN US2002106364-A1.
XX
XX
PD 08-AUG-2002.
XX
XX
PF 09-AUG-2001; 2001US-00927180.
XX
PR 27-JUL-1994; 94US-00281193.
PR 14-APR-1995; 95US-00422106.
PR 14-APR-1995; 95US-00422420.
PR 26-JUN-1995; 95WO-US008069.
PR 08-NOV-1995; 95US-00555568.
PR 09-SEP-1998; 98US-00149988.
PR 06-MAR-2000; 2000US-00519223.
XX
PA (GENY) GENETICS INST INC.
XX
XX Jones S, Tang J;
PI
XX

DR WPI; 2002-739923/80.
DR N-PSDB; ABV73007.
XX
PT Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX
PS Example 4; Page 10-12; 41pp; English.
XX
CC The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a cPLA2/B enzyme (clone 9)
XX
SQ Sequence 752 AA;
Query Match 91.2%; Score 3302.5; DB 5; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVEEGQLILFQNTPRNTWDCILV 60
Db 1 MQFFGRLVNTLSSVTLFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
QY 61 NPNRSQSGFRLLFOLEADALVNPFOYSSQLLPFFYESSPOVLHTEVLQHLTDLIRNHPSW 120
Db 61 SPNPHSGFRLLFOLEADALVNFQFSQSLPFPFESSVQVLHVEVLQHLSDLIHSPSW 120
QY 121 SVLAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDSSEILVELVQYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACOLGQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLQVNNQGLTPLHLACOMGQEMVRVLL 240
QY 241 LCNARCNIMGNGYPIHSAKFESQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNVWGSPGFPIHTAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCNCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRCGCDVSDSTAAGNTALHVAVMNRFDCAIVLLTYGANAGTPEHNTPLHLAISK 360
QY 361 DNEMIKALIVFGAEVDTPEHNTPLHLAISKIGK-LQDLMIHISRAKPAFTILGSMRDEK 419
Db 361 DNEMIKALIVFGAEVDTPEHNTPLHLAISKIGK-LQDLMIHISRAKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGGVKGLIIQLLIIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
Db 421 RIHDLHLCLDGGGVKGLVIIQLLIIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFLKREFEHTKMTDVRKPKVMTLGTLSDRQPA 539
Db 481 AYMRGVYFRMKDEVPFRGSRPYESGPLEEFLKREFEHTKMTDVRKPKVMTLGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQVNLPPAQPDSQDLVWRAARSSGAAPTFRPNRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQVNLPPAQPDSQDLVWRAARSSGAAPTFRPNRFLDGG 600

XX US2002106364-A1.
 XX PD 08-AUG-2002.
 XX PF 09-AUG-2001; 2001US-00927180.
 XX PR 27-JUL-1994; 94US-00281193.
 XX PR 14-APR-1995; 95US-00422106.
 XX PR 14-APR-1995; 95US-00422420.
 XX PR 26-JUN-1995; 95WO-US008069.
 XX PR 08-NOV-1995; 95US-00555568.
 XX PR 09-SEP-1998; 98US-00149988.
 XX PR 06-MAR-2000; 2000US-00519223.
 XX PA (GEMY) GENETICS INST INC.
 XX Jones S, Tang J;
 XX WPI; 2002-739923/80.
 XX DR N-PSDB; ABV73011.
 XX Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
 XX Claim 6; Page 28-30; 4lpp; English.
 XX The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme longer splice variant (clone 19b)
 XX SQ Sequence 688 AA;
 Query Match 99.6%; Score 3606.5; DB 5; Length 688;
 Best Local Similarity 99.7%; Pred. NO. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MOFFGLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
 Db 1 MOFFGLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
 QY 61 NPNRSQSGFRLFQLEADALVNFHOYSQQLPFYESSQVLTHTVQLHLDLIRNHPWS 120
 Db 61 NPNRSQSGFRLFQLEADALVNFHOYSQQLPFYESSQVLTHTVQLHLDLIRNHPWS 120
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDBILVELVOYCHTQMD 180
 Db 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDBILVELVOYCHTQMD 180
 QY 181 VTDYKGETVHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGQEMVRVLL 240
 Db 181 VTDYKGETVHYAVQGDNSQVLQLGRNAVAGLQVNNQGLTPLHLACQLGQEMVRVLL 240
 QY 241 LCNARCINMGPNGYPIHSAKMSQKCAEMIISMDSSQIHSKDPYGCASPLHWAKNAEMA 300
 Db 241 LCNARCINMGPNGYPIHSAKMSQKCAEMIISMDSSQIHSKDPYGCASPLHWAKNAEMA 300

QY 301 RMLLRGCVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLRGCVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVFGAEVDTPNDFGETPTFLASKIGK-LODLMIHISRAKPAFTILGSMRDEK 419
 Db 361 DNVEIMKALIVFGAEVDTPNDFGETPTFLASKIGKLODLMIHISRAKPAFTILGSMRDEK 420
 QY 420 RTHDHLCLDGGGVKGLIIIIQLLIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 479
 Db 421 RTHDHLCLDGGGVKGLIIIIQLLIAEKASGVATKDLFDWVAGTSTGGILALAILHLSKSM 480
 QY 480 AYMRGMYFRMKDEVPGRSGRPYESGLEBEFLKEFEHETKMTDVRPKVMTCTLSDRQPA 539
 Db 481 AYMRGMYFRMKDEVPGRSGRPYESGLEBEFLKEFEHETKMTDVRPKVMTCTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTFFRNGRFLDGG 599
 Db 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLVWRAARSSGAAPTFFRNGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNOQLIRKQANKVKKLSIVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 601 LLANNPTLDAMTEIHEYNOQLIRKQANKVKKLSIVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDCCTDDPGRP 687
 Db 661 WELAKTVFGAKELGKMWVDCCTDDPGRP 688
 RESULT 5
 ADD93407
 ID ADD93407 standard; protein; 784 AA.
 XX AC ADD93407;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human lipid-associated molecule LIPAM-14 polypeptide.
 XX Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
 KW antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;
 KW antinflammatory; thyromimetic; antiallergic; cerebroprotective;
 KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;
 KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
 KW virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
 KW nootropic.
 XX OS Homo sapiens.
 XX WO2003083081-A2.
 XX PD 09-OCT-2003.
 XX PF 27-MAR-2003; 2003WO-US009755.
 XX PR 29-MAR-2002; 2002US-0368722P.
 XX PR 03-MAY-2002; 2002US-0377576P.
 XX PR 05-JUL-2002; 2002US-0393934P.
 XX PR 27-SEP-2002; 2002US-0414269P.
 XX PA (INCY-) INCYTE CORP.
 XX Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;
 PI Baughn MR, Lee EA, Griffin JA, Kable AE, Elliott VS, Chang H;
 PI Lee S, Ramkumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;
 PI Jackson AA;
 XX WPI; 2003-788347/74.
 XX DR N-PSDB; ADD93426.
 XX New LIPAM polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with abnormal expression or activity of LIPAM, e.g.
 PT neuromuscular, immunological, cardiovascular disorders, cancer and/or

Db 301 RMLLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVFGAEVDTNDFTETFLASKIGKQLQDLMHISRARKPAFILGSMRDEKR 420
 Db 361 DNVEIMKALIVFGAEVDTNDFTETFLASKIGKQLQDLMHISRARKPAFILGSMRDEKR 420
 QY 421 THDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKMA 480
 Db 421 THDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKMA 480
 QY 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMTLGTLSDRQPAE 540
 Db 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMTLGTLSDRQPAE 540
 QY 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDDLWRAARSSGAAPTYPFRNGRFLDGG 600
 Db 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDDLWRAARSSGAAPTYPFRNGRFLDGG 600
 QY 601 LANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPW 660
 Db 601 LANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNPW 660
 QY 661 ELAKTVFGAKELGKMVDDCCTDPGRP 687
 Db 661 ELAKTVFGAKELGKMVDDCCTDPGRP 687

RESULT 3
 AAW17848
 ID AAW17848 standard; protein; 688 AA.
 AC AAW17848;
 XX
 DT 07-AUG-1997 (first entry)
 XX Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
 DE Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KW inflammation; inhibitor; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN WO9717448-A2.
 PD 15-MAY-1997.
 XX
 PF 07-NOV-1996; 96WO-US017794.
 XX
 PR 08-NOV-1995; 95US-00555568.
 XX (GEMY) GENETICS INST INC.
 PA Jones S, Tang J;
 XX WPI; 1997-281037/25.
 DR N-PSDB; AAT68826.
 XX
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.
 XX
 PS Claim 12; Page 54-56; 74pp; English.
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839-44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other sPLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host

CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade
 XX
 SQ Sequence 688 AA;
 Query Match 99.6%; Score 3606.5; DB 2; Length 688;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MOPFGLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
 Db 1 MOPFGLVNTFSGVNTLFSNPRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
 QY 61 NPNRSOSGRLFOLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHLDLIRNHPSW 120
 Db 61 NPNRSOSGRLFOLELEADALVNFHOYSQQLLPFYESSQVLHTEVQLHLDLIRNHPSW 120
 QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBCGCTPLHLACRKGDEILVELVQYCHTQMD 180
 Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBCGCTPLHLACRKGDEILVELVQYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
 Db 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
 QY 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQSIHSDKPRYGASPLHWAKNAEMA 300
 Db 241 LCNARCNIIMPNGYPITHSAMKFSQKCAEMIISMDSQSIHSDKPRYGASPLHWAKNAEMA 300
 QY 301 RMLLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLLKRCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVFGAEVDTNDFTETFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 419
 Db 361 DNVEIMKALIVFGAEVDTNDFTETFLASKIGK-LQDLMHISRARKPAFILGSMRDEK 420
 QY 420 RTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 479
 Db 420 RTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 480
 QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMTLGTLSDRQPA 539
 Db 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLEKREFGEHTKMTDVRKPKVMTLGTLSDRQPA 540
 QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDDLWRAARSSGAAPTYPFRNGRFLDGG 599
 Db 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDDLWRAARSSGAAPTYPFRNGRFLDGG 600
 QY 600 LANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
 Db 600 LANNPTLDAMTEIHEYNDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
 QY 660 WELAKTVFGAKELGKMVDDCCTDPGRP 687
 Db 660 WELAKTVFGAKELGKMVDDCCTDPGRP 688

RESULT 4
 ABB82232
 ID ABB82232 standard; protein; 688 AA.
 AC ABB82232;
 XX
 DT 08-JAN-2003 (first entry)
 XX Human cPLA2/B splice variant (clone 19b).
 DE
 XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
 XX antiasthmatic; human.
 OS Homo sapiens.

XX	SQ	Sequence 687 AA;
XX	PD	Query Match
XX	PF	Best Local Similarity 100.0%; Score 3620; DB 2; Length 687;
XX	PP	Mismatches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	PR	08-AUG-2002.
XX	PR	09-AUG-2001; 2001US-00927180.
XX	PR	27-JUL-1994; 94US-00281193.
XX	PR	14-APR-1995; 95US-00422106.
XX	PR	14-APR-1995; 95US-00422420.
XX	PR	26-JUN-1995; 95WO-US008069.
XX	PR	08-NOV-1995; 95US-00555568.
XX	PR	09-SEP-1998; 98US-00149988.
XX	PR	06-MAR-2000; 2000US-00519223.
XX	PA	(GEM) GENETICS INST INC.
XX	PI	Jones S, Tang J;
XX	DR	WPI: 2002-739923/80.
XX	DR	N-PSDB; ABV73010.
XX	PT	Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
XX	PS	Claim 6; Page 23-25; 41pp; English.
XX	CC	The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme longer splice variant (clone 19a)
XX	SQ	Sequence 687 AA;
QY	QY	Query Match 100.0%; Score 3620; DB 5; Length 687;
DB	DB	Best Local Similarity 100.0%; Pred. No. 0;
QY	QY	Mismatches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	DB	1 MQFFGRLVNTFSGVNLFNSNFRVKEVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV 60
QY	QY	1 NPNRSQSGLFQLEADALVNPHOYSSQLLPFYESSPQVLHTEVQLHLTLIRNHPSW 120
DB	DB	61 NPNRSQSGLFQLEADALVNPHOYSSQLLPFYESSPQVLHTEVQLHLTLIRNHPSW 120
QY	QY	121 SVAHLAVALGIRECFHHSHRIISCANCAENEBGCTPLHLACRGKDGGEILVELVQYCHTQMD 180
DB	DB	121 SVAHLAVALGIRECFHHSHRIISCANCAENEBGCTPLHLACRGKDGGEILVELVQYCHTQMD 180
QY	QY	181 VTDYKGETVFHYAVOGDNSQVLQLLGRNAVAGLNQNNQGLTPHLACOLGQBMVRVLL 240
DB	DB	181 VTDYKGETVFHYAVOGDNSQVLQLLGRNAVAGLNQNNQGLTPHLACOLGQBMVRVLL 240
QY	QY	241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSQQIHSDPKRYCASPLHWAKNAEMA 300
DB	DB	241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSQQIHSDPKRYCASPLHWAKNAEMA 300
QY	QY	301 RMLLKRCGNVNSTSAGNTALHVGMNRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB	DB	301 RMLLKRCGNVNSTSAGNTALHVGMNRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
QY	QY	361 DNVEIMKALIVGAEDVTNDPGFTFLASKIGKLQDLMIHSARKPAFILGSMRDEKR 420
DB	DB	361 DNVEIMKALIVGAEDVTNDPGFTFLASKIGKLQDLMIHSARKPAFILGSMRDEKR 420
QY	QY	421 THDHLLCLDGGVGKLIITOLLIAIEKASGVATKOLFDMVAGTSFGGILAILHKSMA 480
DB	DB	421 THDHLLCLDGGVGKLIITOLLIAIEKASGVATKOLFDMVAGTSFGGILAILHKSMA 480
QY	QY	481 YMRGMVPMKDVEFRSGRPYESGLEEFKREFEGHTMTDVVKPKVMLTGTLSRDQPAE 540
DB	DB	481 YMRGMVPMKDVEFRSGRPYESGLEEFKREFEGHTMTDVVKPKVMLTGTLSRDQPAE 540
QY	QY	541 LHFLFRNYDAPETVREPRFNQNVLPPAQSPDQVLRRAARSGAAPTYFRPNRFLDGLL 600
DB	DB	541 LHFLFRNYDAPETVREPRFNQNVLPPAQSPDQVLRRAARSGAAPTYFRPNRFLDGLL 600
QY	QY	601 LANNPILDAMTEHEYNODLIRGOANKYKLSIVVSLGTGSRPOVPVTCVDVFRPSNPW 660
DB	DB	601 LANNPILDAMTEHEYNODLIRGOANKYKLSIVVSLGTGSRPOVPVTCVDVFRPSNPW 660
QY	QY	661 ELAKTVFGAKELGKMVVDDCTDPDGRP 687
DB	DB	661 ELAKTVFGAKELGKMVVDDCTDPDGRP 687
RESULT 2		
ABB82231		
ID	ABB82231	standard; protein; 687 AA.
XX	AC	AB882231;
XX	AC	AB882231;
DT	DT	08-JAN-2003 (first entry)
DE	DE	Human cPLA2/B splice variant (clone 19a).
XX	XX	Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme; antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic; antiasthmatic; human.
KW	KW	
OS	OS	Homo sapiens.
PN	PN	US2002106364-A1.

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 88.6667 Seconds
(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFRLVNTFGVTNLFNS.....GAKELGKMVVDCCTPDGGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3620	100.0	687	2	AAW17847	Aaw17847 Cytosolic
2	3620	100.0	687	5	ABB82231	Abb82231 Human cPL
3	3606.5	99.6	688	2	AAW17848	Aaw17848 Cytosolic
4	3606.5	99.6	688	5	ABB82232	Abb82232 Human cPL
5	3593.5	99.3	784	7	ADD93407	Add93407 Human lip
6	3566.5	98.5	806	5	AAE25968	Aae25968 Human PLA
7	3566.5	98.5	806	8	ADO19776	Ado19776 Human PRO
8	3544.5	97.9	810	8	ABM84355	Abm84355 Human dia
9	3544.5	97.9	810	8	ABM84354	Abm84354 Human dia
10	3302.5	91.2	752	2	AAR83018	Aar83018 Calcium-i
11	3302.5	91.2	752	2	AAW01479	Aaw01479 Calcium-i
12	3302.5	91.2	752	2	AAW13163	Aaw13163 Ca-indepe
13	3302.5	91.2	752	2	AAW17849	Aaw17849 Hamster c
14	3302.5	91.2	752	2	AAW81825	Aaw81825 Chinese h
15	3302.5	91.2	752	5	ABB82215	Abb82215 Calcium i
16	3257	90.0	751	7	ADD46244	Add46244 Rat Prote
17	3257	90.0	751	7	ADE60532	Ade60532 Rat Prote
18	3257	90.0	751	7	ADE55230	Ade55230 Rat Prote
19	3257	90.0	751	7	ADE60536	Ade60536 Rat Prote
20	2723	75.2	667	7	ADM05093	Adm05093 Human pro
21	2084	57.6	394	2	AAW17845	Aaw17845 Cytosolic
22	2084	57.6	394	5	ABB82229	Abb82229 Calcium i
23	1690.5	46.7	401	4	AAW82811	Aaw82811 Human pro
24	1531	42.3	292	2	AAW17846	Aaw17846 Cytosolic
25	1531	42.3	292	5	ABB82230	Abb82230 Calcium i

ALIGNMENTS

RESULT 1

AAW17847
ID AAW17847 standard; protein; 687 AA.
XX
AC AAW17847;
DT 07-AUG-1997 (first entry)
XX
DE Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
XX
KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
inflammation; inhibitor; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO9717448-A2.
XX
PD 15-MAY-1997.
XX
PF 07-NOV-1996; 96WO-US017794.
XX
PR 08-NOV-1995; 95US-00555568.
XX
(GEMY) GENETICS INST INC.
XX
PA Jones S, Tang J;
XX
PI WPI; 1997-281037/25.
XX
DR N-PSDB; AAT68825.
XX
PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX mammalian subject.
XX
PS Claim 12; Page 49-51; 74pp; English.
XX
CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
characterised by activity in the absence of calcium, by activity in a
mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
lack of stimulation by ATP, and by including in its sequence at least one
of the amino acid sequences given in AAW17839- 44). It is an
alternatively spliced variant of another isolated polypeptide (AAW17845)
and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes
(AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
thought to be involved in the release of arachidonic acid in specific
tissues. Recombinant sPLA2/B polypeptides produced in transformed host
cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
drugs which inhibit the arachidonic acid cascade

[illegible]

Qy	37	RVRBEGQLILFONTRRWDCVLVNPRNSQSGFRLFQLELEAD--ALWNFHQYSSQLLPF	94
Db	204	RAKEEEL---KPKPLYHLAIIYNNENKYSVLSFSLKHLADVVALCERCENPELFRV	266
Qy	95	YESSPQV---LHTEVLQHLTDLIRNHPSPWSVAHLAVELGIRECFHH---SRIISCANCAE	148
Db	261	FPKNVNIKDYLHT-----IFHELDRNMTWKSVHSSKIGLLEYFENMKHKLKYLNLIV	315
Qy	149	NBEGCTPLHLACKGDGILVELVOYCHTQMDVTDYKGETVFHVAVQDMSOVLQLL--G	206
Db	316	QPEGLSPLMIAVQNTQIETVSWMLDH--GADINILSSQGNVLHVAAATSSGDILKILWET	374
Qy	207	RNAVAGLNQVNNQGITPLHLACQLGKQEMVRVLLLCNARCINIMGPNG-----Y	255
Db	375	KKCEWIMNCTDSNGYTPAVVA-----IINACTI.SNCOTI.RGFEGGSSSDSTOMAN	428

Q810Q6 PRELIMINARY: PRT: 1021 AA.

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun. Release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirska R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003550; AAF50194.3; -;
DR HSSP; Q60778; 10Y3.
DR FlyBase; FBgn0036053; CG6718.
DR GO; GO:0003824; F.catalytic activity; IEA.
DR GO; GO:0045733; F.nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 4.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00246; ANK; 6.

DR PROSITE; PSS0088; ANK_REPEAT; 3.
DR PROSITE; PSS0297; ANK_REPEAT; 1.
KW ANK repeat.
SQ SEQUENCE 877 AA; 96862 MW; C9DC2CD6C282869B CRC64;
Query Match 32.1%; Score 1163.5; DB 2; Length 877;
Best Local Similarity 31.9%; Pred. No. 2e-79;
Matches 257; Conservative 135; Mismatches 248; Indels 165; Gaps 12;
QY 17 LFSNPFPRKEVAVADYTSDDRVREGQLILFQNTNRTWDCVLNPNRSQSGFRFLQLEL 76
DB 40 LFAPPF-----NSSNEKRAVVEIILQRTSD-----SNTTSFSLVRSV 78
QY 77 EADALVNHOYSSQLLPYESSQVILHTEVLOHLTLRNHPHSVAHLAVELGREGPH 136
DB 79 QQAEERENAFLORLPVPVSVKYEYNYNGLOKACDALADNPSTLSHLIAYFNLDVYIS 138
QY 137 HSRIISCANCAENBEGCTPLHLACRKGGEILVELVQYCHTQMDVTDYKGVTFVHAVQG 196
DB 139 NPKMLQCVDDQADATLMSFPQLAIKQHMWVKALLPL--SKLEHLDINSNSVFHYAA-S 195
QY 197 DNSQVLQLGRNAVAGLNQVANNQGLTPLHLACQLGKQEMVRVLLLCNRCNIMGNGYPI 256
DB 196 TTKEIINLIIDKSTVNLNHLNSDGYTPLHVACLADKPNVVKALLAGANVNL--NANDI 252
QY 257 HSAMFQSGKGAEMIISMDSQIHSKDPRIYGASPLHAKNAEMARMLLKRCNCNVNSTSA 316
DB 253 RKVYKTSAPTTSVSSFLRTNVSPLYQDMKYGGTPLHWCSSRETLHALIMEGCDVNATNPD 312
QY 317 GNTALHVGVMNRPCATVLLTHGANADARGHNTPLHLAMSNDVEMIKALIVFGARV 376
DB 313 GRTALHVMVARNRFEVCTVLLAHDAEIDVLDKGDNAALHIAIEKKLVPIVQCLVFGCDI 372
QY 377 DTPNDFGETP-----TFLASKIG----- 394
DB 373 NLKNKGKGTPRHVMGNDSAGNKNKDBILYILHSVGAKRCKDTGSKPCPGCNAGNYGIPP 432
QY 395 ----KLQDLMHSR----- 411
DB 433 EAPESVEQREHIEHMLATTSRQMMGGFLNAAANGILEKQQAQKPVVDTEKELKGQSIM 492
QY 412 ----LGSMR----- 424
DB 493 DALLGMFTTKVNADEMKENSDDSLASQKSAVSSPQLPSPSPPIAAIEGDKPYGRGR 552
QY 425 LCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTGTGGLIALAILHSKSNWYMG 484
DB 553 LCLDGGGIRGLVLVQMLLEIEKLSRTPIIHFWDIAGTGTGGLIALALCGCKTMRQCMG 612
QY 485 MYFRMKDEVFRGSRPYESGPLEEFKREFGHTKTDYRKPKVMTLTLSDRQPAELHLIF 544
DB 613 LYLRMKEQCFVGSRYNSEFFESILKDNLGEFNVMTDIKPKIMVTGVNADRKPDVLDHLF 672
QY 545 RNYDAPETVR---EPRENQVNLPPAOPSDOLVRAARSAGAAFTYPRPNRGRFLDGGGL 601
DB 673 RNYTSASDILGIVTPINNRR---PPQPSQGLVRAARATGAATGAATGAATGAATGAAT 729
QY 602 ANNPITDAMTEIHEYNODLIRKQANKVKKLSIVVSLGTGRSPQVPTCVDFRPSNPWE 661
DB 730 ANNPITDAMTEIHEYNMRLSAGRESEALPVSVMNSLGTGHIPVTELKIDIDVFRPES 789
QY 662 LAKTVFGAKELGKMWVDCTPDGR 686
DB 790 TAKLAYGISTIGNLLVDQATCSDGR 814
RESULT 11
QYKUD4
ID Q7KUD4
AC Q7KUD4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

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Db 600 YKSTATFQPLTVQGHEDDLVGVTRPPRRKRVYDDEQLVWRAARSSGAAPTFRPM 659
QY 593 GREFDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCYD 652
Db 660 GREFDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCYD 719
QY 653 VFRPSNPWELAKTVFGAKELGKMWVDCCTDPDG 685
Db 720 VFRPSNPWELAKTVFGAKELGKMWVDCCTDSG 752

RESULT 9
Q7Q2U1 PRELIMINARY; PRT; 879 AA.
AC Q7Q2U1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EbiP3359 (Fragment).
GN Name=ebiG3359; ORFNames=ENSANGG00000002698;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008968; EAA13225.1; -.
DR HSSP; P20749; 1K1B.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000560; HisAc phosphatase.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS0088; ANK REPEAT; 3.
DR PROSITE; PS0297; ANK REP REGION; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW ANK repeat.
FT NON_TER 1
FT NON_TER 879
SQ SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;

Query Match 32.2%; Score 1164; DB 2; Length 879;
Best Local Similarity 32.1%; Pred. No. 1.8e-79;
Matches 260; Conservative 134; Mismatches 269; Indels 146; Gaps 9;

QY 21 PPRVKEVAVADYTSRDRREGQLILFQNTPNR-----TWDCVLNPNRS--OSGRLFLQ 73
Db 11 PNKQVEKNESYINLPVQKNESMRIFAPNPNPDKLVYVEILRPHSETINTSYSLR 70
QY 74 LELEADALNVHFOYSSQLLPFYESSQVILHTEVLQHLTLIRNHPSPSWVAHLAVELGIRE 133
Db 71 ATTQSAAEKFEAFHQRLPELVKIVREMYNINGLQKLCVDLIDNPSSWLAHVAFYNLTD 130
QY 134 CFHHSIIISCANCAENEGCTPLHLACRKGDEGLVVELVQYCHTQMDVTDYKGETVHYA 193
Db 131 YISNPSIIDFLDYAEYSEMMTPLOQAVKANNIEFVKALIQSNQCNLEHLDKNSNVHYA 190
QY 194 VQGDNSQVLQLGRNAVAGINNVNNOGLTPLHLACQLGKQEMVRVLLLCNARNINMGPN 253
Db 191 A-STTKEMINMLTAKTSNLNHCNTDGYTPLHLACLADKPCVKALLAGADTNKVA-RG 248
QY 254 YPIHSAMKFSQKCAEMITSMDSQTHSKDPRYGASPLHWAKNAEMRMLLKRCGVNST 313
Db 249 AGTSYSKSISSNVADFLVS-NPNKFLTQDMKHGGTPLHWSSSRVLSNLSIERGCDVNLV 307
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QY 314 SSAGNTALHGVGNRFRDCAIVLLTTCANADARGEHNTPLHLAMSKDNVEMIKALIVFG 373
Db 308 NFNGQPTPLHVMARDLECVALLADAEIDVDVNSGNTPLHIAVEKKLPIVQCLVVF 367
QY 374 AEVDTPNDPGEPTFL-----ASKIGKLDLMH----- 401
Db 368 ADFNKENKDGKTPRHLVGKDDSGSKSMILYILHVGAKRCPEKSGKPPGCAAGTYNG 427
QY 402 -----ISRA 405
Db 428 IPPAQPETTEQREHIQOVLARTTTKSHRNSVPVSLISNTIRATIPERERPEVKTVDVSQE 487
QY 406 RKPAPFILGSM-----RDEKRTHD----- 423
Db 488 RKGASMDALLSNFMSKVEAASKPTSPTSTSSSLKECAGSGGORTSRPRSSCEAGSGE 547
QY 424 -----HLCLDGGGVKGLIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALILHSK 477
Db 548 SYNGRGLLCLDGGGIRGLVLAQMLLEIENLAQTPIVHLFDWIAGTSTGGILALALCGCK 607
QY 478 SMAYMGMYFRMKDEVFRGSRPYESOPLEFLKREGEHTKMTDVRKPKVMLTGTLSDRQ 537
Db 608 TMKQCNCILYLRMKDQAFVGSRPYPSPDQETVLKEQLGEFTVMSDIKHPRLMVTGVMA DRK 667
QY 538 PAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOLVWRAARSSGAAPTFRPNGRFLD 597
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QY 598 GGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCYDVFPRPS 657
Db 728 GGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCYDVFPRPD 787
QY 658 NPWELAKTVFGAKELGKMWVDCCTDPDG 686
Db 788 SIWATAKVAYGISTITLLVDQATASDGR 816

RESULT 10
Q9VT60 PRELIMINARY; PRT; 877 AA.
AC Q9VT60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6718-PA.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fouts C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
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QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEGILLVELVOYCHTQMD 180
Db 121 SLAHVAVEIGLSEKPHGILSLNSTECDCGSTPLHLACKCKGNCLOELVEEQCARLD 180
QY 181 VTDYKGETVFHYAVOGDINSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQVVRVLL 240
Db 181 IADQNGEIVYHAAQONPRVIEILCSVPSGVNHSNNNETPLHVACELGKTELVALL 240
QY 241 LCNARCNIMGNGYPIHSAKFSQKGCAMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 RCHARCDIIGKDGYPITHAMKYSQCEVBAILDVSASQLHARDPRYQATPIHAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
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QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRAK-----PAFILGSM 415
Db 361 DQLELIKALMVFGADVEQHNDFGETPGLTAARSSKGFDFVYVSTALSGMLVPQDVTDFR 420
QY 416 REKETHHLLCLDGGGVKGLIIQLLIAEKASGVATKDLFDWVAGTSGTGILALAILH 475
Db 421 EDGLRVKORLLCLDGGGIRGLVLMQLLIAEKAAGRPIRELFDMVSGTSGTGILALAIH 480
QY 476 SKSMAYMRGMYFRMKDEVFGRGSRPYESGPLEFLKREFGHTKMTDVRKPKVMLTGTLS 535
Db 481 GMPBSVRCCLYFRMKNEVPHGRSPYESGPLEFLKREFGHTKMTDVRKPKVMLTGTLS 540
QY 536 ROPAEHLHFRNYDAPETVREPRFNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNGRF 595
Db 541 RHPAEHLHFRNYDPPETDHEPPYKSVASPRVTPAEQLVWRAARSSGAAPTYLRPMGRF 600
QY 596 LDGGLANNPTLDAMTEIHEYNOGLIRKQANKVKLSIVSLGTRSPQVPTCVDPVR 655
Db 601 LDGGLSNNTLDAMTEIHEYNTCLKKGMAGVKKLGIVSLGTGKPPQISVSGVDVFR 660
QY 656 PSNPVELAKTVGAKELGKVVDCCTDPDG 685
Db 661 PSNPVEWMTVVGARELGKVVDCCTDSOG 690

RESULT 8

OSNWY0
ID Q6NWY0 PRELIMINARY; PRT; 818 AA.
AC Q6NWY0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE ZGC:77476.
GN ORFNames=ZGC:77476;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067375; AAH67375.1; -;
DR HSSP; P20749; 1KJB.
DR ZFIN; ZDB-GENE-040426-2079; ZGC:77476.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKTRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401P8EA9 CRC64;
Query Match 54.6%; Score 1977.5; DB 2; Length 818;
Best Local Similarity 50.5%; Pred. No. 2.1e-141;
Matches 380; Conservative 122; Mismatches 182; Indels 69; Gaps 4;
QY 1 MQPFGRLVNTSGVNTLFSNPRVKEVAVADYTSDDRVRESCQLILFQNTNRTWDCVLV 60
Db 1 MOFLGRILDTSSVSSLSFNPRVVDVQLSDYNGKILHQEGRLALYNQSQSQCWDCLL 60
QY 61 NPNRSQSGFLFQLEADALVNFHOYSQQLPFYESSQVLTHTVQLHTDLIRNHPSW 120
Db 61 CPESPSVALRMFOVASEEDAMNWFQYALKLRFPEMLRPPLKPEMLQPIVDCVNHDP 120
QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEGILLVELVOYCHTQMD 180
Db 121 SSAHIAVDTLGRDCLKHNVILSQMN-SRDAQQTPLHLACERGDVGCVRLEECQARTD 179
QY 181 VTDYKGETVFHYAVOGDINSQVQLLGRNAVAGLQVNNQGLTPLHLACOLGQKQVVRVLL 240
Db 180 VKDKNGETPMCAAKQDSALIIIEVLCAQACAGVNSLNAAGETPMHIACTRLGVEVVKGL 239
QY 241 LCNARCNIMGNGYPIHSAKFSQKGCAMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 240 AGGARCDIMGNGFPPIHTAMKFSKCAAILSSPNQLLAEDPVYGGTPLHWAKTAMS 299
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 300 RLILDRGCNVNYSKTESPLHILTKRGRFEAAVMTLLTHGADANIRGQDNTALHLAMKL 359
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK----- 395
Db 360 DNMDLIKALMVFGADVEVHNDVGETPGLTAARSSKGNKVLNMLCSVGVRECHPPSLN 419
QY 396 -----LQDLMHIS-----RAKPAFALIGSMRDEKRTDHLCLDGGGVKGLI 437
Db 420 SPTHSLRKAPPGICGFDIMQVAVATAMSRGFEADGLKTKGNKMDRLCLDGGGKGLV 479
QY 438 IFQLLIAEKASGVATKDLFDWVAGTSGTGILALAILHSKSWAYRMGYFRMKDEVFRS 497
Db 480 LIQLLIALEKEAGRPIRELFDMVSGTSGTGILALAILVHGSMEYLRCLYFRMKDEVFRS 539
QY 498 RPYESGPLEFLKREFGHTKMTDVRKPKVMLTGTLSRQPAELHLFRNYDAPETVREPR 557
Db 540 RPYESGPLEFLKREFGHTKMTDVRKPKVMLTGTLSRQPAELHLFRNYDAPETVREPR 599
QY 558 FNQNVNLRPPAOP-----SDQLVWRAARSSGAAPTYFRN 592

DR	PRINTS; PRO1415; ANKYRIN.	DT	25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DR	SMART; SM00248; ANK; 6.	DE	25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DR	PROSITE; P550088; ANK REPEAT; 4.	DE	MGC83523 (protein.
DR	PROSITE; P550297; ANK_REPEAT REGION; 1.	GN	Name=MGC83523;
KW	ANK repeat; Hydrolase; Lipid degradation; Repeat.	OS	Xenopus laevis (African clawed frog).
FT	REPEAT 150 180 ANK 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	REPEAT 184 214 ANK 2.	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
FT	REPEAT 218 247 ANK 3.	OC	Xenopodinae; Xenopus.
FT	REPEAT 250 280 ANK 4.	OX	NCBI_TaxID=8355;
FT	REPEAT 285 311 ANK 5.	RN	[1]_TaxID=8355;
FT	REPEAT 315 344 ANK 6.	RP	SEQUENCE FROM N.A.
FT	REPEAT 348 377 ANK 7.	RC	TISSUE=Eye;
FT	ACT SITE 464 464 Potential.	RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
SQ	SEQUENCE 751 AA; 83582 MW; 393BBADA7PCC99B CRC64;	RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Query Match		RA	Richardson P.
Best Local Similarity 89.7%; Score 3257; DB 1; Length 751;		RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;		RL	Dev. Dyn. 225:384-391(2002).
		RN	[2]
QY	1 MOFFGRLVNTFSGVTLNFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60	RP	SEQUENCE FROM N.A.
Db	1 MOFFGRLVNTLSSVTNLFNPFRAKEVSLADYASSERVREEGQLILQNASRTWDCVLV 60	RC	TISSUE=Eye;
QY	61 NPNRSQSGRLPQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Db	61 SPNPNQSDFLPQLESEADVLNFFQYSQQLPPFYESSQVLHVEVLQ-LTDLIRNHPSW 119	RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
QY	121 SVAHLAVALGIRECFHSHSIISCANCAENEGCTPLHLACRGDGIIVELVQYCHTQMD 180	RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Db	120 TVTHLAVALGIRECFHSHRIITCANSTENEGCTPLHLACRGDSILVELVQYCHAQND 179	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
QY	181 VTDYKGETVFHVAQGDNSQVLQIGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240	RA	Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
Db	180 VTDNKGTAFAHVAQGDNPQVLQKKNASAGLNQVNNQGLTPLHLACONGQEMVRVLL 239	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
QY	241 LCNARNCINMGPGYPIHSAKMSQKCAEMIISMDSSQIHSKDPDPRYGASPLHWAKNAEMA 300	RA	Brownstein M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Db	240 LCNARNCINMGPGFPIHTAKMSQKCAEMIISMDSNQIHSKDPDPRYGASPLHWAKNAEMA 299	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
QY	301 RMLLKRCGNVNTSSAGNTALHGVWRNFDCAIVLLTGANADARGEHNTPLHLAMSK 360	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Db	300 RMLLKRCGDVNTSSAGNTALHVAVTNRNFDCAIVLLTGANADARGEHNTPLHLAMSK 359	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
QY	361 DNVEIMKALIVGAEDVTDNDGETTFLASKIGK-LQDLMHISRAKPAFILGSMRDEK 419	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Db	360 DNVEWKALIVGAEDVTDNDGETTFLASKISKQLQDLMFVSRARKEPAFILSSMRDEK 419	RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
QY	420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSQM 479	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Db	420 RTHDHLCLDGGVGKGLVIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSQM 479	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
QY	480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMTLGTLSRQPA 539	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Db	480 AYMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVKPKVMTLGTLSRQPA 539	RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
QY	540 ELHLFRNYDAPETVREPNQNVNLRPPAQPDSOLVRAARSGGAAPTYFRNGRFLDGG 599	RA	Jones S.J., Marra M.A.;
Db	540 ELHLFRNYDAPVREPRCTPNINLKPPTQADQLVRAARSGGAAPTYFRNGRFLDGG 599	RT	"Generation and initial analysis of more than 15,000 full-length human
QY	600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Db	600 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659	RN	[3]
QY	660 WELAKTVFGAKELGKMWVDCCTDPDR 686	RP	SEQUENCE FROM N.A.
Db	660 WELAKTVFGAKELGKMWVDCCTDPDR 686	RC	TISSUE=Eye;
RESULT 7		RA	Klein S., Gerhard D.S.;
Q6DDKO	PRELIMINARY; PRT; 756 AA.	RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
AC	Q6DDKO;	DR	EMBL; BC077558; AAH77558.1; -.
DT	25-OCT-2004 (TReMBLrel. 28, Created)	DR	GO; GO:0003824; F:catalytic activity; IEA.
		DR	GO; GO:0045735; F:nutrient reservoir activity; IEA.
		DR	InterPro; IPR002110; ANK.
		DR	InterPro; IPR002641; Patatin.
		DR	Pfam; PF00023; Ank; 7.
		DR	Pfam; PF01734; Patatin; 1.
		DR	PRINTS; PR01415; ANKYRIN.
		DR	SMART; SM00248; ANK; 7.
		DR	PROSITE; PS50088; ANK_REPEAT; 3.
		DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.
		KW	ANK repeat.
		SQ	SEQUENCE 756 AA; 84303 MW; C0278741CCAS2A71 CRC64;
		Query Match	
		Best Local Similarity 61.1%; Score 2210.5; DB 2; Length 756;	
		Matches 413; Conservative 120; Mismatches 152; Indels 5; Gaps 2;	
QY	1 MOFFGRLVNTFSGVTLNFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60	QY	1 MOFFGRLVNTFSGVTLNFSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db	1 MDLFGRIFTVTSVAVTNLFNPNKYREVPLSEYSGSSCLQEDGEMLYRNRTAKSLDCVLV 60	Db	1 MDLFGRIFTVTSVAVTNLFNPNKYREVPLSEYSGSSCLQEDGEMLYRNRTAKSLDCVLV 60
QY	61 NPNRSQSGRLPQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120	QY	61 NPNRSQSGRLPQLELEADALVNFHQSOLLPPFYESSQVLHTEVLQHLTDLIRNHPSW 120
Db	61 NPSSPQNAVRLPQLESEPEALCRFOYAVKLPFPYESSRKGCLCLETLOQLTDCIRHPNW 120	Db	61 NPSSPQNAVRLPQLESEPEALCRFOYAVKLPFPYESSRKGCLCLETLOQLTDCIRHPNW 120

RP SEQUENCE FROM N.A.
RC TISSUE=Testis; DOI=10.1073/pnas.242603899;
RX PubMed=12477932; Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altshuler S.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081916; AAH81916.1; -;
DR InterPro; IPR002110; ANK.
DR Pfam; PF002023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hypothetical protein.
SQ SEQUENCE 807 AA; 89555 MW; 1B9018AE1B2D252F CRC64;

Query Match 90.3%; Score 3268; DB 2; Length 807;
Best Local Similarity 83.7%; Pred. No. 1.4e-239;
Matches 621; Conservative 29; Mismatches 36; Indels 56; Gaps 1;

QY 1 MQFFGRLVNTFGVNLFSNPRFRVEKVAADYTSSDRVREEQQLILFQNTNRTWDCVLV 60
DB 1 MQFFGRLVNTLSSVTLNFSNPRFRVEKVSADYASSERVEEQQLILQNASNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLEADALVNFQYSSQLLPFYESSQVLTHTVQLHTLIRNHPSW 120
DB 61 SPRNFQSGRLFOLEADALVNFQYSSQLLPFYESSQVLTHTVQLHTLIRNHPSW 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEECTPLHLACRGDGEILVELVQYCHTQMD 180
DB 121 TVTHLAVALGIRECFHHSRIISCANSTENEECTPLHLACRGDGEILVELVQYCHAQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNQLTPLHLACQLGQKQEMVRVLL 240
DB 181 VTDNRGETAFHYAVQGDNPQVLQLGKNASAGLNVNQLTPLHLACQKQEMVRVLL 240

QY 241 LCNARCNMGNGPYPIHSAKFSQKCAEMIISMDSQIHSDKPRYGASPLHWAKNAEMA 300
DB 241 LCNARCNMGNGPGFPIHTAMKFSQKCAEMIISMDSQIHSDKPRYGASPLHWAKNAEMA 300

QY 301 RMLLRKGCNVNSTSSAGNTALHGVNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSSAGNTALHGVNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVMEMIKALIVFAEVDTPNDFGCTPTFLASKIGK----- 395
DB 361 DNVMEMIKALIVFAEVDTPNDFGCTPTFLASKIGK----- 395

QY 396 -----LQDLMHISRAKPAFILGSMRDEKRDTHD 424
DB 396 -----LQDLMHISRAKPAFILGSMRDEKRDTHD 424

DB 421 VSTEQSSAAGPHPPFSLDRTPPTISLNNLEQLDMLPVSRAKPAFILSSMRDEKRDTHD 480
QY 425 LLCIDGGGVKGLIITQLLIAIEKASGVATKDLFDWAGTGTGGIILALATLHKSMAWNRG 484
DB 481 LLCIDGGGVKGLIITQLLIAIEKASGVATKDLFDWAGTGTGGIILALATLHKSMAWNRG 540
QY 485 MYFRMKDVFGRSGPYESGPLEEFKLRFBGHTKMTDVRKPKVMTGTLSDRQPAELHLF 544
DB 541 VFYFRMKDVFGRSGPYESGPLEEFKLRFBGHTKMTDVRKPKVMTGTLSDRQPAELHLF 600
QY 545 RNYDAPETVREPRFNQNVNLRPPAPQSPDOLVWRAARSSGAAPTYFRPNRGFLDGGLLANN 604
DB 601 RNYDAPEAVREPRCTPNLNKPTOPADQLVWRAARSSGAAPTYFRPNRGFLDGGLLANN 660
QY 605 PTLDAWTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDFVFRSPNWEAK 664
DB 661 PTLDAWTEIHEYNQDMIRKQGNKVKLSIVVSLGTGKSPQVPVTCVDFVFRSPNWEAK 720
QY 665 TVFGAKELGKMWVDCCTDPDGR 686
DB 721 TVFGAKELGKMWVDCCTDPDGR 742

RESULT 6
PA26 RAT ID PA26 RAT STANDARD; PRT; 751 AA.
AC P97570;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ledenson J., Turk J.;
RT "Pancreatic islets express a Ca2+-independent phospholipase A2 enzyme that contains a repeated structural homologous to the integral membrane protein binding domain of ankyrin.";
RL J. Biol. Chem. 272:11118-11127(1997).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids. It has been implicated in normal phospholipid remodeling, nitric oxide-induced or vasopressin-induced arachidonic acid release and in leukotriene and prostaglandin production. May participate in fas mediated apoptosis and in regulating transmembrane ion flux in glucose-stimulated B-cells.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver, heart and skeletal muscle.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U51898; AAC53136.1; -;
DR HSSP; O60778; 10Y3.
DR RGD; 628867; Pla2g6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 6.
DR


```
QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
D 1 MOFFGRLVNTSSVNTLFSNPRFVKEVSLTDYVSSERVREEGQLILLQNVSNRTWDCVLV 60
QY 61 NPNRSQSGRFLQLEADALVNFHOYSOLLPPYESSQVLHTEVLOHLDLIRNHP 120
D 61 SPNPFQSGRFLQLESEADALVNFQSSQLPPFYESSQVLHTEVLOHLDLIRNHP 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIILVELVQYCHTQMD 180
D 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSILLVELVQYCHAQMD 180
QY 181 VTDYKGETVHVAVQGDNSQVLQLGRNAVAGLNVQNNQGLTPLHLACOLGHOEVRVLL 240
D 181 VTDNKGETAFAHYAVQGDNPQVLQLLGNKASAGLNVQNNQGLTPLHLACMKGQEMVRVLL 240
QY 241 LCNARCNIMGPNVGYPIHSAKFOSQKCAEMIISDSSOIHSDKPRYGASPLHWAKNAEWA 300
D 241 LCNARCNIMGPGFFPIHTAMKFSQKCAEMIISDMSNOIHSDKPRYGASPLHWAKNAEWA 300
QY 301 RMLLKRGCVNSTSGAGNTALHVGVRNRFDCAIIVLLTHGANADARGHGNTPHLAMSK 360
D 301 RMLLKRGCDVDSTSSGNTALHVAVMNRFDVCMVLLTYGANAGARGEHGNTPHLAMSK 360
QY 361 DNVMEMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFIFLGSNRDEK 419
D 361 DNMEMVKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFIFLGSNRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWVAGTSGGILALAILHKS 479
D 421 RSHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWVAGTSGGILALAILHKS 480
QY 480 AYMRGMYFRMKDEVRGSRPYESGPLEEFKKEFGEHTKMTDVRPKVMTGTLSDRQPA 539
D 481 AYMRGYVFRMKDEVRGSRPYESGPLEEFKKEFGEHTKMTDVRPKVMTGTLSDRQPA 540
QY 540 ELHLFRNVDAPTVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPYFRPNRPLDGG 599
D 541 ELHLFRNVDAPVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPYFRPNRPLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLRKQKANKVKSIVSVSLGTGRSPQVPTCYDVRPNP 659
D 601 LLANNPTLDAMTEIHEYNDLRKQKANKVKSIVSVSLGTGRSPQVPTCYDVRPNP 660
QY 660 WELAKTVFGAKELGKXWVDCCTDPDGR 686
D 661 WELAKTVFGAKELGKXWVDCCTDPDGR 687
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RESULT 3
Q7TPX2

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ID Q7TPX2 PRELIMINARY; PRT; 752 AA.
AC Q7TPX2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus..
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAH52845.1; -.
DR HSSP; P07207; 1078.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Pacatin.
DR Pfam; PF000023; ANK; 6.
DR Pfam; PF01734; Pacatin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14A AFC CRC64;
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Query Match 90.9%; Score 3289.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 2,9e-241;
Matches 621; Conservative 29; Mismatches 36; Indels 1; Gaps 1;

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QY 1 MOFFGRLVNTSGVNTLFSNPRFVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
D 1 MOFFGRLVNTSSVNTLFSNPRFVKEVSLTDYVSSERVREEGQLILLQNVSNRTWDCVLV 60
QY 61 NPNRSQSGRFLQLEADALVNFHOYSOLLPPYESSQVLHTEVLOHLDLIRNHP 120
D 61 SPNPFQSGRFLQLESEADALVNFQSSQLPPFYESSQVLHTEVLOHLDLIRNHP 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEIILVELVQYCHTQMD 180
D 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSILLVELVQYCHAQMD 180
QY 181 VTDYKGETVHVAVQGDNSQVLQLGRNAVAGLNVQNNQGLTPLHLACOLGHOEVRVLL 240
D 181 VTDNKGETAFAHYAVQGDNPQVLQLLGNKASAGLNVQNNQGLTPLHLACMKGQEMVRVLL 240
QY 241 LCNARCNIMGPNVGYPIHSAKFOSQKCAEMIISDSSOIHSDKPRYGASPLHWAKNAEWA 300
D 241 LCNARCNIMGPGFFPIHTAMKFSQKCAEMIISDMSNOIHSDKPRYGASPLHWAKNAEWA 300
QY 301 RMLLKRGCVNSTSGAGNTALHVGVRNRFDCAIIVLLTHGANADARGHGNTPHLAMSK 360
D 301 RMLLKRGCDVDSTSSGNTALHVAVMNRFDVCMVLLTYGANAGARGEHGNTPHLAMSK 360
QY 361 DNVMEMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFIFLGSNRDEK 419
D 361 DNMEMVKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMHISRARKPAFIFLGSNRDEK 420
QY 420 RTHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWVAGTSGGILALAILHKS 479
D 421 RSHDHLCLDGGVKGVLIIQLLIIAEKASGVATKDLFDWVAGTSGGILALAILHKS 480
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D 481 AYMRGYVFRMKDEVRGSRPYESGPLEEFKKEFGEHTKMTDVRPKVMTGTLSDRQPA 540
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[6]
SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clump M., Smink L.J., Anscoough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Suleston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull L., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fullon R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latraile P., Layman D., Ozersky P., Rohlfing T.,
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RA Wilson R., Bedell J.A., Haller L.W., Mardis E., Waterston R.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
CC It has been implicated in normal phospholipid remodeling, nitric
CC oxide-induced or vasopressin-induced arachidonic acid release and

in leukotriene and prostaglandin production. May participate in
fas mediated apoptosis and in regulating transmembrane ion flux in
glucose-stimulated B-cells.
-!- FUNCTION: Isoform ankryn-IPLA2-1 and isoform ankryn-IPLA2-2,
which lack the catalytic domain, are probably involved in the
negative regulation of iPLA2 activity.
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a carboxylate.
-!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
-!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
bound. Isoform SH-IPLA2 is cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
Name=LH-IPLA2;
IsoId=O60733-1; Sequence=Displayed;
Name=SH-IPLA2;
IsoId=O60733-2; Sequence=VSP_000278;
Name=Ankryn-IPLA2-1;
IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
Name=Ankryn-IPLA2-2;
IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
-!- TISSUE SPECIFICITY: Four different transcripts were found to be
expressed in a distinct tissue distribution.
-!- SIMILARITY: Contains 7 ANK repeats.

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or send an email to license@isb-sib.ch.

EMBL; AF064594; AAC97486.1; -
EMBL; AF102988; AAD41722.1; -
EMBL; AF102988; AAD41723.1; -
EMBL; AF117692; AAD30424.1; -
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EMBL; AF117679; AAD30424.1; JOINED.
EMBL; AF117680; AAD30424.1; JOINED.
EMBL; AF117681; AAD30424.1; JOINED.
EMBL; AF117682; AAD30424.1; JOINED.
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EMBL; AF116265; AAF34728.1; JOINED.
EMBL; AF116266; AAF34728.1; JOINED.
EMBL; AL080187; CAB45768.1; ALT_INIT.
EMBL; AY522921; AAR92478.1; -
EMBL; AL022322; CAA18446.1; -
EMBL; BC036742; AAB36742.2; -
EMBL; BC051904; AAB51904.1; -

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 111.667 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFGLVNTFGVTNLFN.....GAKELGKVMVDCCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3566.5	98.5	806	1 PA26 HUMAN	O60733 homo sapien
2	3299.5	91.1	752	1 PA26 MOUSE	P97819 mus musculus
3	3289.5	90.9	752	2 Q7TPE2	O77819 mus musculus
4	3272	90.4	807	2 Q9JK61	O9JK61 mus musculus
5	3268	90.3	807	2 Q66HD1	O66HD1 rattus norv
6	3257	90.0	751	1 PA26 RAT	P97570 rattus norv
7	2210.5	61.1	756	2 Q6DDK0	O6DDK0 xenopus lae
8	1977.5	54.6	818	2 Q6NMY0	O6NMY0 brachydanio
9	1164	32.2	879	2 Q7Q2U1	O7Q2U1 anopheles g
10	1163.5	32.1	877	2 Q9VT60	O9VT60 drosophila
11	1163.5	32.1	887	2 Q7KUD4	O7KUD4 drosophila
12	742	20.5	386	2 Q8MR13	O8MR13 drosophila
13	647.5	17.9	1071	2 Q20500	O20500 caenorhabdi
14	634.5	17.5	1023	2 Q62398	O62398 caenorhabdi
15	629.5	17.4	1021	2 Q81006	O81006 caenorhabdi
16	458	12.7	762	2 Q95YD2	O95YD2 caenorhabdi
17	357.5	9.9	501	2 Q9N5L3	O9N5L3 caenorhabdi
18	338	9.3	843	2 P97582	P97582 rattus norv
19	338	9.3	1219	2 Q8C8R3	O8C8R3 mus musculus
20	332	9.2	1863	2 Q723L5	O723L5 homo sapien
21	332	9.2	3924	1 ANK2 HUMAN	O01484 homo sapien
22	324.5	9.0	1004	2 Q7JNZ0	O7JNZ0 caenorhabdi
23	324.5	9.0	1786	2 Q17344	O17344 caenorhabdi
24	324.5	9.0	1809	2 Q17487	O17487 caenorhabdi
25	324.5	9.0	1815	2 Q17488	O17488 caenorhabdi
26	324.5	9.0	1841	2 Q8MGX0	O8MGX0 caenorhabdi
27	324.5	9.0	1867	2 Q17486	O17486 caenorhabdi
28	324.5	9.0	2039	2 Q17489	O17489 caenorhabdi
29	324.5	9.0	6994	2 Q17343	O17343 caenorhabdi
30	324.5	9.0	6994	2 Q17490	O17490 caenorhabdi
31	320	8.8	1549	2 Q24241	O24241 drosophila

32	320	8.8	1549	2	Q9V4B1	Q9V4B1 drosophila
33	311.5	8.6	820	2	Q8JHU3	Q8JHU3 brachydanio
34	311	8.6	1501	2	Q7QKD3	Q7QKD3 anopheles g
35	310	8.6	1009	2	Q8SWY2	Q8SWY2 drosophila
36	310	8.6	1159	2	Q9NCP8	Q9NCP8 drosophila
37	310	8.6	1571	2	Q7KU92	Q7KU92 drosophila
38	305.5	8.4	792	2	Q7Q172	Q7Q172 anopheles g
39	304	8.4	525	2	Q9TYS0	Q9TYS0 caenorhabdi
40	302	8.3	786	2	Q9ERK0	Q9ERK0 mus musculus
41	301	8.3	1136	2	Q9N180	Q9N180 bos taurus
42	300	8.3	1762	2	O88521	O88521 rattus norv
43	299	8.3	1614	2	Q7TIG6	Q7TIG6 brachydanio
44	298	8.2	2622	2	O70511	O70511 rattus norv
45	297.5	8.2	1726	2	Q8VC68	Q8VC68 mus musculus

ALIGNMENTS

RESULT 1
PA26 HUMAN STANDARD: PRT: 806 AA.
AC O60733; O75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonyms=IPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancreatic islets;
RX MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616 (1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99260933; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RA Ansoorge W., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.;
DT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

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R:David, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
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A:Map position: 8p11.2-8p11.2
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C:Keywords: alternative splicing; phosphoprotein
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F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
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F:828-1382/Region: spectrin binding
F:1383-1881/Domain: 55K #status predicted <DOM3>

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DB 336 LDHLTPL-----HVA-----HCGHRVAKVLLDKGAKPNSRALNGFTPLHIACK 380
QY 162 KGDGEILVELVQYCHTQMD-----VTDYKGET 188
DB 381 KKHVRVM-ELLALKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKVET 439
QY 189 VFHYAVQGDNSQVLQLGRNAVAGLNOVNNQGLTPLHLACOLGKQRMVRVLLLCNARCNI 248
DB 440 PLHMAARAGHTEVAKYLLQNK-AKVNAKAKDDQTPHLCAARIGHTNNVKLLLENANPNL 498
QY 249 MGPNGY-----PIHSAMKFSQKGCAMIISM 274
DB 499 ATTAGHTPLHIAAREGHVETVLALLEKEASQACMTKKGFTPLHVAKYKVRVAELLER 558
QY 275 DSSQIHSKDPRYGASPLHWA---KNAEMARMLLKRCNVNNTSSAGNTALHVGVMNRFD 331
DB 559 DAHP--NAAGKNGLTPLHVAHHNLDIVKLLPRGGSPHSPAWNGYTPPLHTAAKQNV 616

QY 332 CAIVLLTHGANADARGEHGNTPHLHMSKDNVEMIKALIVFGAEVDPNDFGETPTFLAS 391
DB 617 VARSLLQYGGSSANAESVQGVTPHLHAAQBGHAEWVALLLSKQANGNKGKSGITPLHLVA 676
QY 392 KIG 394
DB 677 QEG 679

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T42714
ankyrin 3, splice form 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42714
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42714
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C:Keywords: alternative splicing

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QY 180 DVTYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLQKQEMRVYL 239
Db 476 EAKAKDDQTPLHISARLGKADIVQQLQQG-ASPNAATTSGVTPHLAAREGHEDVAAPL 534

QY 240 LLCNARNCTMGNGY-PIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWA---K 295
Db 535 LDHGASLSITTKGFTPLHVAARYKLEVASLLLOKSASP--DAAGKSGLTPLHVAARYD 592

QY 296 NAEAMRLILKRCNVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPH 355
Db 593 NOKVALLLLDQASPHAAKNGYTPHIAAKNQMDIATSLLEYGADANAVTROGIAVH 652

QY 356 LAMSKDNVEMIKALIVFGAEVDTNPFGETPTFLAS---KIGKLDLM-----HISRARKP 408
Db 653 LAAQEGHVDVMSLLSRNANVLSNKSGLTPLHLAAQEDRVNVAEVLVNOGAHVDAQTQM 712

QY 409 AFILGSMRDEKTRTHLLCLDGGVKGILLIQLLIAEKASGVATKDLFDWVAGTSTGGI 468
Db 713 GY-----TPLHVG-C-HYGNIK---IVNFLQHSKAVNAKTKN-----GY 747

QY 469 LALAILHKSMAVMRGMVFRMKDEVFRGSRPYE---SGPLEEFKREFGEHTKMTDVRK- 524
Db 748 TAL-----HQAAQQGHTHIINVLLQNNASPNELTVNGNTALAIARRLG-YISVVDTLKV 800

QY 525 --PKVMLTGTLSDROPAPLHLFRNYDAPETVRE 555
Db 801 VTEEIMTTTITEK-----HKMNVPETMNE 825

RESULT 10
T42715
ankyrin 3, splice form 3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42715
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1943 <PET>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710550; PIDN:AAB01606
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
```

```
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1940 <PET>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 834/1
A:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1940;
Best Local Similarity 24.7%; Pred. No. 3e-14; Indels 69; Gaps 18;
Matches 112; Conservative 81; Mismatches 191;

QY 124 HLAVELG----IRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVQYCHTQM 179
Db 421 HVAAPFGHVNIVSOLMHH-----GASPTTNVGRGTALHWAARSQGAQVRYLVQ-DGAQV 475

QY 180 DVTYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLQKQEMRVYL 239
Db 476 EAKAKDDQTPLHISARLGKADIVQQLQQG-ASPNAATTSGVTPHLAAREGHEDVAAPL 534

QY 240 LLCNARNCTMGNGY-PIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWA---K 295
Db 535 LDHGASLSITTKGFTPLHVAARYKLEVASLLLOKSASP--DAAGKSGLTPLHVAARYD 592

QY 296 NAEAMRLILKRCNVNNTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGNTPH 355
Db 593 NOKVALLLLDQASPHAAKNGYTPHIAAKNQMDIATSLLEYGADANAVTROGIAVH 652

QY 356 LAMSKDNVEMIKALIVFGAEVDTNPFGETPTFLAS---KIGKLDLM-----HISRARKP 408
Db 653 LAAQEGHVDVMSLLSRNANVLSNKSGLTPLHLAAQEDRVNVAEVLVNOGAHVDAQTQM 712

QY 409 AFILGSMRDEKTRTHLLCLDGGVKGILLIQLLIAEKASGVATKDLFDWVAGTSTGGI 468
Db 713 GY-----TPLHVG-C-HYGNIK---IVNFLQHSKAVNAKTKN-----GY 747

QY 469 LALAILHKSMAVMRGMVFRMKDEVFRGSRPYE---SGPLEEFKREFGEHTKMTDVRK- 524
Db 748 TAL-----HQAAQQGHTHIINVLLQNNASPNELTVNGNTALAIARRLG-YISVVDTLKV 800

QY 525 --PKVMLTGTLSDROPAPLHLFRNYDAPETVRE 555
Db 801 VTEEIMTTTITEK-----HKMNVPETMNE 825

RESULT 11
T42713
ankyrin 3, splice form 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42713
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; MUID:95340633; PMID:7615634
A:Accession: T42713
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1943 <PET>
A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710550; PIDN:AAB01606
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
```


RESULT 5

T33857
hypothetical protein D1037.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33857
R:Ledwith, J.; Biewald, T.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of *C. elegans* cosmid D1037.
A:Reference number: Z21424
A:Accession: T33857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-468 <LED>
A:Cross-references: EMBL:AF106592; PIDN:AAC78490.1; GSPDB:GN00019; CESP:D1037.5
A:Experimental source: strain Bristol N2; clone D1037
C:Genetics:
A:Gene: CESP:D1037.5
A:Map position: 1
A:Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 9.0%; Score 324.5; DB 2; Length 468;
Best Local Similarity 27.0%; Pred. No. 1.4e-17;
Matches 110; Conservative 74; Mismatches 164; Indels 59; Gaps 16;

Qy 286 YGASPLHWAKNAEMARMLLKRCNVNSTSSAGNTALHVGVMRN-----RFDCAIVLLTHG 340
Db 44 YDLSVITWLN--LRFLISRYCR-----SENVCNHLEALMNAARYGNTDLLYKLYIH 94

Qy 341 ANADARGEHGNTPHLAMSKDNKVMIKALIVFGAEVD---TPNDFGETPTFLASKIGKLQ 397
Db 95 IDLRMTDETGNTHAMHVAVMNQKIVRLVVLCAPCQIKWIKNNGLSTELCTDKKISE 154

Qy 398 DLMHISRARKP--AF-----ILGMEDEKRTDHD-LICLDGGGVKGLIIQLLIA 444
Db 155 DFKSLDNPSPSPGAFVDVDSYNNVLASEKKQKPEPVLALDDGGGIRAVITIQMLIH 214

Qy 445 IEKASGVATKDLDFWAGTATGCGILALAI-LHKSMAVMRMGYFRMKDEVF-RGSR--P 499
Db 215 IDYLLGGKLVKELDDIAGTSCGGVITLLSTNNRIETRKLILDMRDRVPIRGADKAVP 274

Qy 500 YESGPLEEFLKREF--GEHTKMTDVRKPKVMTGLTSDRQPAELHLPNY--DAPETVRE 555
Db 275 KYSSNGMEYIARHVTWEDSKWSSIKGRHAIVTVADTRMVPQPLLFRSYRPEMPEACE 334

Qy 556 P-RFNQNVNLRPPAQSPDLVWRAARSSGAAPTFRPNGRFLDGGLLANNPTLDMATEIH 614
Db 335 HYKP-----LDPTKVELWKTURCTAAYPFESFNGLSDGGLANNPTLALISDFP 385

Qy 615 EYNODLIRKGOANKVK-----KLISIVSLGTGRSPQVPVTCVDV 653
Db 386 LTNK--LEKSPAKSSSERENGNWKIGCVISLGTGVPTFEKIDGIDL 430

RESULT 6

T15347
ankyrin-related unc-44 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
R:Gattung, S.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of *C. elegans* cosmid B0350.
A:Reference number: Z18332
A:Accession: T15347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2039 <GNT>
A:Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PFI:15346
A:Accession: T15346
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE', 1958-1959, 'E'>
32, 'S', 2034-2035, 'GSPTRRSVEEEHHSHOHEDHEGST' <GA>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1
A:Accession: T15344
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KW', 1903-1905, 'NLRADESSPS', 1916-1917, 'QRSTIVAESTSQQVPE', 1934-1935, 'E'>
<GA>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1
A:Accession: T15345
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE',
PTRSRVPEEHRRHSQHEDHEGST' <GA>
A:Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
R:Ocsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontarakulpoor,
J. Cell Biol. 129, 1081-1092, 1995
A>Title: An ankryrin-related gene (unc-44) is necessary for proper axonal guidance in Caer
A:Reference number: A57282; MUID:95263663; PMID:7744957
A:Accession: A57282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'B',
'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: B57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'B',
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTSRVPEEHRRHS', 1984-1985, 'EDEGS', 1986-1987, 'E'
A:Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
C:Genetics:
A:Gene: CESP:unc-44
A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1719/2; 1979/2;
C:Superfamily: ankryrin; ankryrin repeat homology
F:164-192/Domain: ankryrin repeat homology <AN04>
F:358-390/Domain: ankryrin repeat homology <ANI>
F:391-423/Domain: ankryrin repeat homology <AN11>

	Query Match	9.0%; Score 324.5; DB 2; Length 2039;
	Best Local Similarity	24.1%; Pred. No. 1.4e-16; Matches 129; Conservative 77; Mismatches 207; Indels 123; Gaps 16;
Qy	147	AENEEGCTPLHLACRGDGEILVELVQYCHTQMVDYKGTVFHVAVQGDNSQVLQLLG 206
Dd	420	ATTESGLTPLHVAFMGAINIVYLLOQ-GANPDVETVGETGPLHLAARANTDVVRVLI 478
Qy	207	RNAVAGLNQVNQGLTPLHLACQLQGKBQEWVRVLLLCNARCNTMGPNGY-PIHSAMKPSQK 265
Dd	479	RNG-AKVDAQARELQTPHLIASRLGNTDIVILLQAGANSNATTRDNYSPFLHAAKEGQE 537
Qy	266	GCAEMIITSDSSQTHSKD-----PRYGASPLHWAK---NAEMARMLLKRCGNVNSTSSAGN 318
Dd	538	EVAIGILL-----HNADKTLLTKKGFTPLHLASKYGNLEVVLRLLERGTFPDIEGKNQV 591
Qy	319	TALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSNDNVEMIKALI VFGEAEVDT 378
Dd	592	TPLHVAHYNDKYVAMLLEN GASAKAAKNGYTPHLIAAKNQMEIASTLLQFKADPNA 651
Qy	379	PNDFGETTFLASKIGKLQDLMLHI SRARKPAF ILGSMRDKERKTHDLLCLDCGGVKGILI I 438
Dd	652	KSRAGFTPLHLSAQBGHKE-----ISGLL- 675
Qy	439	IQLLIAEKASGVATKDLFDWVAGTSGTGII ALAILHKSMAVMRCGMVFMKDEVFRGR 498
Dd	676	-----TENGSDVGAK-----ANNGLTAMHLC-----AQEDHV----- 702

Db 466 VPABQGSAAHPHPSFLERAPPPISLNLEQLDMHISPAKPAFILGSMRDEKTHDHL 525
QY 426 LCLDGGVKGGLIIIIQLLIAEKASGATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 485
Db 526 LCLDGGVKGGLIIIIQLLIAEKASGATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 585
QY 486 YPRMKDEVPRSGRPYESGPLEBFLKRECEHTKMTDVRKPKVMTGTLSDROPABELHLFR 545
Db 586 YPRMKDEVPRSGRPYESGPLEBFLKRECEHTKMTDVRKPKVMTGTLSDROPABELHLFR 645
QY 546 NYDAPETVREPRFNQVNLPRPAQSDQLVRAARSSGAAPTYFRPNRGFLDGGLLANP 605
Db 646 NYDAPETVREPRFNQVNLPRPAQSDQLVRAARSSGAAPTYFRPNRGFLDGGLLANP 705
QY 606 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVPRPNPHELAKT 665
Db 706 TLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQVPVTCVDVPRPNPHELAKT 765
QY 666 VFGAKELGMVVDCTDPPGR 686
Db 766 VFGAKELGMVVDCTDPPGR 786

RESULT 2
T22327
hypothetical protein F47A4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22327
R:Mortimore, B.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19549
A:Accession: T22327
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1071 <WTL>
A:Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F47A4
A:Experimental source: clone F47A4
C:Genetics:
A:Gene: CESP:F47A4.5
A:Map position: X
A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 17.9%; Score 647.5; DB 2; Length 1071;
Best Local Similarity 27.0%; Pred. No. 1.5e-42;
Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

QY 69 FRLFQLELEADALVNFHQSOLLPEYSSPQVLTHTVL----OHLTDLIRNHPSSVAH 124
Db 315 FSLFRATDKKDLMLLHLCDEKSLFTSLDMTMRADILRSKIEELVQIRLKPHYMH 374
QY 125 LAVELGIRECFHSRI-----ISCANCAENBEGCTPLHLACRGDGBILVELVQY 174
Db 375 VALATDRDLDFSDGMKTKMNETLEPPESQLRCLCHTENCYPVHALTMDROKIVERLLEL 434
QY 175 CHTQMDVTDYKGETVHYAVQDGNQSVQLLGRNAVAG---LNQVNNQGLTPLHLACQLG 231
Db 435 DPTLCFTCDKAGNVVHHV---NSSFCAQIIWDRCPASQHFIDERNMQSQSPLEAVSTA 491
QY 232 KQEMVRVLLCNARCNIMGYPYHSAMKFSQKGAEMIISM-----DSS 277
Db 492 KPLVATFL-----IGKGAKFTRGDRNELFVAMTSKNAQSVVEVVLTDKP 535
QY 278 QIHSQDPKRYGASPLHWAKNAEMARMLLK-----GNVNSTSAGNTALHVGVMRNRFOCA 333
Db 536 ETANERDALGNASIAHVALYKESINALLNRKVELGLDIDVKNAGETALLPTTRKPDLL 595
QY 334 IVLLT---HGANADARGEHNTPLHAMS-----KONVEMIKALIVFGAEVDPNDPFGT 385
Db 596 PLLVTLYHAGANNATDPGNTALHKSAAALVDAKKISLCVFLISAGSNPNKINLRGES 655
QY 386 PTFLASKICKLODLWHISPA---RKPATILG-----SMRDE----- 418

Db 656 PRHLAASL-QNOEMLAIIKAAAGATRCPKGYGCGRSNCRHDCSSAEDEYEETLOKIRIGNE 714
QY 419 -----KRTDHLCLCGGKGLIIIIQLLIAEKASGVA 452
Db 715 SDYEKTEFTASEKLNIQDTLQDSRRGKAKVKNLISMDGGGIRGLVIIQTLLIAEERLQDD 774
QY 453 TKDLFDWVAGTSTGGILALAILHKSMAVMRGMFRMKDEVFRG--SRPYESGPLEBFLKR 511
Db 775 IFKYPDWSAGTSGSLIMAGLATGKSLREMOQOTYLLLKDRVPDGMPPYDTVQLBKFQD 834
QY 512 EFGHTKMTDVRKPKVMTGTLSDROPABELHLFRNYDAPETVREPRFNQVNLPRPAQPS 571
Db 835 QFGTGT-WBEIPYPRLMISAVNSEKLPVLEWARYNPKADV-----APEPK 881
QY 572 DQLVRAARSSGAAPTYFRPN-GRPLDGLLANPDLTLDAMTEIHEYNQDLIRKQANKVK 630
Db 882 EMLMALRRSTAAPVLFKPSEDRYIDGGIISNNPALDLMSEVHAYNRELQLSGRKSDAV 941
QY 631 KLSIVVSLGTGRSPQVPVTCVDVFR--PSNPWELAKTVFGAKELGMVVDCTDPPGR 687
Db 942 QMNVLVSEFTG---QIPSTVIETLISIDNSPLQSIKTI---KNLAAMFIDQATASEGAP 994

RESULT 3
T26261
hypothetical protein W07A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26261; T26892
R:Baaham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20184
A:Accession: T26261
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1023 <WTL>
A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CAB04932.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone W07A8
R:Ainscough, R.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20281
A:Accession: T26892
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-1023 <W12>
A:Cross-references: EMBL:AL021489; PIDN:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone Y44A6C
C:Genetics:
A:Gene: CESP:W07A8.2
A:Map position: 5
A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 701/2

Query Match 17.5%; Score 634.5; DB 2; Length 1023;
Best Local Similarity 24.2%; Pred. No. 1.5e-41;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

QY 37 RVREGQILFQNTPNRTWDCVLVNPNSQSGFRFLQLELEAD--ALNVFHOYSQQLPFF 94
Db 204 RAKEBEEL---KNKPLYHLAITLVNENNEKYVMSLFRSHKLDADVVALCERCENPELFRV 260
QY 95 YESSPOV---LHTEVLQHLTDLIRNHPSSVAHLAVELGIRECFH---SRIISCANCAE 148
Db 261 FPKNVNIDKYLHT-----IFHEDRNMTWKSVHISKSKIGLLEYFENMKHKLKKYLNLI 315
QY 149 NEEGCTPLHLACRGDGBILVELVQYCHTQMDVTDYKGETVHYAVQDGNQSVQLL--G 206
Db 316 QPEGLSPLMIAVQNTQIETVSWMLDH-CADINILSSEGNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNNQGLTPLHLACQLGQKQBMVRVLLCNARCNIMGPNG-----Y 254
Db 375 KKCETMINQTSNGYTPAVVA-----LINACLNSCQTLRGFGGIGQSSDSTQMAN 424
QY 255 PIHSAMKFSQ--KGCAEMIISMDSSQIHSKDPKRYGASPLHWAKNAEMARMLLK---GCN 309

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 19.6667 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MQFFGLVNTFSGVTNLFNS.....GAKELGKMVVDCTDPDGR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3566.5	98.5	851	2 T12503	hypothetical prote
2	647.5	17.9	1071	2 T23237	hypothetical prote
3	634.5	17.5	1023	2 T26261	hypothetical prote
4	332	9.2	3924	2 S37431	ankyrin 2, neurona
5	324.5	9.0	468	2 T33857	hypothetical prote
6	324.5	9.0	2039	2 T15347	ankyrin-related un
7	320	8.8	1549	2 T13940	ankyrin - fruit fl
8	296	8.2	4377	2 A55575	ankyrin 3, long sp
9	294.5	8.1	1765	2 T42714	ankyrin 3, splice
10	294.5	8.1	1940	2 T42715	ankyrin 3, splice
11	294.5	8.1	1943	2 T42713	ankyrin 3, splice
12	294.5	8.1	1961	2 T42716	ankyrin 3, splice
13	294	8.1	1856	2 B35049	ankyrin 1, erythro
14	294	8.1	1880	2 A35049	ankyrin 1, erythro
15	294	8.1	1881	1 SJHUK	ankyrin 1, erythro
16	285	7.9	1848	2 S37771	ankyrin, erythrocy
17	285	7.9	1862	2 I49502	ankyrin - mouse
18	282.5	7.8	397	2 T46445	hypothetical prote
19	278.5	7.7	1411	2 S30355	alpha-latroinsecto
20	269.5	7.4	1265	2 T02131	hypothetical prote
21	268	7.4	456	2 T24442	hypothetical prote
22	264	7.3	1423	1 I37275	death-associated p
23	250.5	6.9	1435	2 T32930	hypothetical prote
24	249	6.9	791	2 T42691	hypothetical prote
25	244	6.7	247	2 D84448	probable ankyrin [
26	242.5	6.7	1401	2 S11527	alpha-latrotoxin p
27	242	6.7	2437	2 AE2149	transmembrane prot
28	239.5	6.6	426	2 AE2149	hypothetical prote
29	235.5	6.5	355	2 E82354	patatin-related pr

30	234.5	6.5	633	2 T27499	hypothetical prote
31	231	6.4	934	1 H71274	probable ankyrin -
32	229.5	6.3	368	2 T18184	ankyrin repeat pro
33	223	6.2	2524	2 A35844	Xotch protein - Af
34	221.5	6.1	907	2 I50404	p50B/p97 (lyt-10)
35	221.5	6.1	1062	2 T14151	inv protein - mous
36	220.5	6.1	1062	2 T30255	inversin - mouse
37	220	6.1	1184	2 T00253	gene Ankhzn protei
38	219	6.0	2531	2 A46019	notch-1 protein -
39	215	5.9	2555	2 A40043	notch protein homo
40	214.5	5.9	2531	2 S18188	notch protein homo
41	213.5	5.9	679	2 J71615	phospholipase A2 (
42	213.5	5.9	782	2 GC7284	transcription fact
43	213.5	5.9	933	2 S17233	hypothetical prote
44	208.5	5.8	606	2 AC2508	hypothetical prote
45	207	5.7	2352	2 T30201	Notch homolog prot

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFp434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12503
R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17527
A:Status: preliminary
A:Accession: T12503
A:Molecule type: mRNA
A:Residues: 1-851 <ANS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFzp434A102
C:Genetics:
A:Note: DKFp434A102.1

Query Match 98.5%; Score 3566.5; DB 2; Length 851;
Best Local Similarity 92.3%; Pred. No. 1.5e-273;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

QY	1	MQFFGLVNTFSGVTNLFNSPFRVKEVAVADYTS	SDRVREEGQLILFQNTPNRTWDCVLV	60
DB	46	MQFFGLVNTFSGVTNLFNSPFRVKEVAVADYTS	SDRVREEGQLILFQNTPNRTWDCVLV	105
QY	61	NPRNSQSGFRLPQLEADALVNFHQYSSQLLPFY	ESSPQVLHTEVQLHLDLIRNHP	120
DB	106	NPRNSQSGFRLPQLEADALVNFHQYSSQLLPFY	ESSPQVLHTEVQLHLDLIRNHP	165
QY	121	SVAHLAVELGIRECFHSHRIISCANCAENEECT	PLHLACRKGDEILVELVOYCHTOMD	180
DB	166	SVAHLAVELGIRECFHSHRIISCANCAENEECT	PLHLACRKGDEILVELVOYCHTOMD	225
QY	181	VTDYKGETVFHVAVOGDINSQVLQLGRNAVAGI	NQVNNQGLTPLHLACOLGQEMVRVLL	240
DB	226	VTDYKGETVFHVAVOGDINSQVLQLGRNAVAGI	NQVNNQGLTPLHLACOLGQEMVRVLL	285
QY	241	LCNARCNIIMPNGYPIHSAKFQSKGCAEMIIIS	MBSSQIHSKDPDPRYGASPLHWAKNAEMA	300
DB	286	LCNARCNIIMPNGYPIHSAKFQSKGCAEMIIIS	MBSSQIHSKDPDPRYGASPLHWAKNAEMA	345
QY	301	RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAI	VILLTHGANADARGEHNTPLHLAMSK	360
DB	346	RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAI	VILLTHGANADARGEHNTPLHLAMSK	405
QY	361	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI	GK-----	395
DB	406	DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI	GKRLVTRKAILTLRTVGAECFFPIHG	465
QY	396	-----	-----LQDLMHISPAKPAFTILGSMRDEKRTDHL	425

Db	517	HTKMTUVKPKVMTGLTSLDRQPAELHLFRNYDAPEVIREPRENQINILKPTQPADQLV	576
Qy	181	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNOQLIRKQANKVKKLSIV	240
Db	577	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNOQLIRKQANKVKKLSIV	636
Qy	241	VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDDPGR	291
Db	637	VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDDPGR	687

Search completed: May 26, 2005, 14:21:57
 Job time : 11.7676 secs

Query Match		96.1%;	Score 1471;	DB 2;	Length 752;	
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;			
Matches		277;	Conservative	8;	Mismatches 6;	Indels 0; Gaps 0;
QY	1	LODLMHISRKAPAFILSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD	60			
Db	397	LODLMPISRARKPAFILLSSMRDEKRIHDHLLCLDGGGVKGLVIIQLLIAIEKASGVATKD	456			
QY	61	LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERFGRSPYBSGPLEBFLKREFGE	120			
Db	457	LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERFGRSPYBSGPLEBFLKREFGE	516			
QY	121	HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV	180			
Db	517	HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV	576			
QY	181	WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	240			
Db	577	WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	636			
QY	241	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	291			
Db	637	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	687			
RESULT 14						
US-08-555-5688-2						
; Sequence 2, Application US/085555688						
; Patent No. 5976854						
; GENERAL INFORMATION:						
; APPLICANT: Jones, Simon						
; APPLICANT: Tang, Jim						
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B						
; NUMBER OF SEQUENCES: 25						
; CORRESPONDENCE ADDRESS:						
; ADDRESSEE: Genetics Institute, Inc.						
; STREET: 87 CambridgePark Drive						
; CITY: Cambridge						
; STATE: Massachusetts						
; COUNTRY: U.S.A.						
; ZIP: 02140						
; COMPUTER READABLE FORM:						
; MEDIUM TYPE: Floppy disk						
; COMPUTER: IBM PC compatible						
; OPERATING SYSTEM: PC-DOS/MS-DOS						
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)						
; CURRENT APPLICATION DATA:						
; APPLICATION NUMBER: US/08/555,568B						
; FILING DATE:						
; CLASSIFICATION: 435						
; ATTORNEY/AGENT INFORMATION:						
; NAME: Brown, Scott A.						
; REGISTRATION NUMBER: 32,724						
; TELECOMMUNICATION INFORMATION:						
; TELEPHONE: (617) 498-8224						
; TELEFAX: (617) 876-5851						
; INFORMATION FOR SEQ ID NO: 2:						
; SEQUENCE CHARACTERISTICS:						
; LENGTH: 752 amino acids						
; TYPE: amino acid						
; TOPOLOGY: linear						
; MOLECULE TYPE: protein						
US-08-555-5688-2						
Query Match		96.1%;	Score 1471;	DB 2;	Length 752;	
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;			
Matches		277;	Conservative	8;	Mismatches 6;	Indels 0; Gaps 0;
QY	1	LODLMHISRKAPAFILSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD	60			
Db	397	LODLMPISRARKPAFILLSSMRDEKRIHDHLLCLDGGGVKGLVIIQLLIAIEKASGVATKD	456			
US-08-555-5688-2						
Query Match		96.1%;	Score 1471;	DB 3;	Length 752;	
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;			
Matches		277;	Conservative	8;	Mismatches 6;	Indels 0; Gaps 0;
QY	1	LODLMHISRKAPAFILSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD	60			
Db	397	LODLMPISRARKPAFILLSSMRDEKRIHDHLLCLDGGGVKGLVIIQLLIAIEKASGVATKD	456			
QY	61	LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERFGRSPYBSGPLEBFLKREFGE	120			
Db	457	LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERFGRSPYBSGPLEBFLKREFGE	516			
QY	121	HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV	180			
Db	517	HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV	576			
QY	181	WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	240			
Db	577	WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	636			
QY	241	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	291			
Db	637	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	687			
RESULT 15						
US-09-519-223-2						
; Sequence 2, Application US/09519223						
; Patent No. 6274140						
; GENERAL INFORMATION:						
; APPLICANT: Jones, Simon						
; APPLICANT: Tang, Jim						
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B						
; NUMBER OF SEQUENCES: 25						
; CORRESPONDENCE ADDRESS:						
; ADDRESSEE: Genetics Institute, Inc.						
; STREET: 87 CambridgePark Drive						
; CITY: Cambridge						
; STATE: Massachusetts						
; COUNTRY: U.S.A.						
; ZIP: 02140						
; COMPUTER READABLE FORM:						
; MEDIUM TYPE: Floppy disk						
; COMPUTER: IBM PC compatible						
; OPERATING SYSTEM: PC-DOS/MS-DOS						
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)						
; CURRENT APPLICATION DATA:						
; APPLICATION NUMBER: US/09/519,223						
; FILING DATE:						
; CLASSIFICATION:						
; PRIOR APPLICATION NUMBER: US/08/555,568						
; FILING DATE:						
; ATTORNEY/AGENT INFORMATION:						
; NAME: Brown, Scott A.						
; REGISTRATION NUMBER: 32,724						
; TELECOMMUNICATION INFORMATION:						
; TELEPHONE: (617) 498-8224						
; TELEFAX: (617) 876-5851						
; INFORMATION FOR SEQ ID NO: 2:						
; SEQUENCE CHARACTERISTICS:						
; LENGTH: 752 amino acids						
; TYPE: amino acid						
; TOPOLOGY: linear						
; MOLECULE TYPE: protein						
US-09-519-223-2						
Query Match		96.1%;	Score 1471;	DB 3;	Length 752;	
Best Local Similarity		95.2%;	Pred. No. 3.3e-160;			
Matches		277;	Conservative	8;	Mismatches 6;	Indels 0; Gaps 0;
QY	1	LODLMHISRKAPAFILSGMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD	60			
Db	397	LODLMPISRARKPAFILLSSMRDEKRIHDHLLCLDGGGVKGLVIIQLLIAIEKASGVATKD	456			
QY	61	LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERFGRSPYBSGPLEBFLKREFGE	120			
Db	457	LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERFGRSPYBSGPLEBFLKREFGE	516			
QY	121	HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV	180			
Db	517	HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV	576			
QY	181	WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	240			
Db	577	WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	636			
QY	241	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	291			
Db	637	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	687			

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QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 584 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 643
QY 181 WRAARSSGAAPTYFRPNRGLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 644 WRAARSSGAAPTYFRPNRGLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 703
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 704 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 754

RESULT 11
US-08-281-193-2
; Sequence 2, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-281-193-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.3e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLHMSRARKPAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LODLMPISRARKPAFILSSMRDEKRIHDHLCLDGGGVKGLVILQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHKSMAVMRGVYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAILHKSMAVMRGVYFRMKDEVFRGSRPYESGPLEBFLKREFGE 516
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRGLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRGLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687
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RESULT 12
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-422-106-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.3e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLHMSRARKPAFILSGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LODLMPISRARKPAFILSSMRDEKRIHDHLCLDGGGVKGLVILQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHKSMAVMRGVYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120
DB 457 LFDWVAGTSTGGILALAILHKSMAVMRGVYFRMKDEVFRGSRPYESGPLEBFLKREFGE 516
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRGLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRGLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
DB 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 13
US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-735-716-2
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; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-519-223-23

Query Match 100.0%; Score 1531; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGVGKGLIIQLLIAIEKASGVATKD 60
Db 397 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGVGKGLIIQLLIAIEKASGVATKD 456

QY 61 LFDWAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
Db 457 LFDWAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 516

QY 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 180
Db 517 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 576

QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
Db 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 636

QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
Db 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 9
US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TANG, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:

; APPLICATION NUMBER: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 1531; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGVGKGLIIQLLIAIEKASGVATKD 60
Db 397 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGVGKGLIIQLLIAIEKASGVATKD 456

QY 61 LFDWAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
Db 457 LFDWAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 516

QY 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 180
Db 517 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRNQNVNLRPPAQPSDQLV 576

QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
Db 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 636

QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
Db 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 10
US-09-949-016-10948
; Sequence 10948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10948
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10948

Query Match 99.5%; Score 1524; DB 4; Length 819;
Best Local Similarity 100.0%; Pred. No. 2.9e-166;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGVGKGLIIQLLIAIEKASGVATKD 60
Db 464 LQDLMHISRARKPAFILGSMRDEKTRTHDLLCLDGGVGKGLIIQLLIAIEKASGVATKD 523

QY 61 LFDWAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 120
Db 524 LFDWAGTSTGGILALAILHSHKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFKREFGE 583
```

;
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 09-Aug-2001
; APPLICATION NUMBER: US/09/927,180
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 1531; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRAKPAFILGSMRDEKRTDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 60
Db |||||
QY 396 LQDLMHISRAKPAFILGSMRDEKRTDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 455
Db |||||
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
Db |||||
QY 456 LFDWAGTSTGGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
Db |||||
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQIV 180
Db |||||
QY 516 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQIV 575
Db |||||
QY 181 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
Db |||||
QY 576 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 635
Db |||||
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 292
Db |||||
QY 636 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 687
Db |||||

RESULT 7
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-23

Query Match 100.0%; Score 1531; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRAKPAFILGSMRDEKRTDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 60
Db |||||
QY 397 LQDLMHISRAKPAFILGSMRDEKRTDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 456
Db |||||
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
Db |||||
QY 457 LFDWAGTSTGGILALAILHKSMAVMRGYFRMKDEVFRGSRPYESGPLEEFLKREFGE 516
Db |||||
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQIV 180
Db |||||
QY 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQIV 576
Db |||||
QY 181 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
Db |||||
QY 577 WRAARSSGAAPTYFRPNRFLDGLGGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 636
Db |||||
QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 292
Db |||||
QY 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDDPGRP 688
Db |||||

RESULT 8
US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

Db 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292

RESULT 4

US-08-555-568B-21
; Sequence 21, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-21

Query Match 100.0%; Score 1531; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVGKGLIIQLLIAIERKASGVATKD 60
Db 396 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVGKGLIIQLLIAIERKASGVATKD 455

QY 61 LFDWAGTSTGGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKEEFG 120
Db 456 LFDWAGTSTGGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKEEFG 515

QY 121 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQLV 180
Db 516 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQLV 575

QY 181 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 240
Db 576 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 635

QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
Db 636 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 5

US-09-519-223-21
; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-21

Query Match 100.0%; Score 1531; DB 3; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.5e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVGKGLIIQLLIAIERKASGVATKD 60
Db 396 LQDLMHISRARKPAFILGSMRDEKTRTHDHLCLDGGVGKGLIIQLLIAIERKASGVATKD 455

QY 61 LFDWAGTSTGGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKEEFG 120
Db 456 LFDWAGTSTGGILALAILHSKSMAYMRGMVFRMKDEVERGSRPYESGPLEEFLKEEFG 515

QY 121 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQLV 180
Db 516 HTKMTDVRKPKVMTGTLSDROPAPAEHLFRNYDAPETVREPRFNQNVNLRPPAQPDSQLV 575

QY 181 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 240
Db 576 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIV 635

QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
Db 636 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 687

RESULT 6

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive

QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292
DB 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292
RESULT 2
US-09-519-223-19
; Sequence 19, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-19

Query Match 100.0%; Score 1531; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 LODLMIHISRAKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
DB 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292
DB 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292
RESULT 3
US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
; US-09-927-180-19

Query Match 100.0%; Score 1531; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LODLMIHISRAKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 1 LODLMIHISRAKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
DB 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFKKEFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP 292

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 10.7676 seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLHISRARPAFILGSM.....GAKELGKVVVDCCTDPGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCRUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfilees1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1531	100.0	292	3	US-09-519-223-19
3	1531	100.0	292	4	US-09-927-180-19
4	1531	100.0	687	2	US-08-555-568B-21
5	1531	100.0	687	3	US-09-519-223-21
6	1531	100.0	687	4	US-09-927-180-21
7	1531	100.0	688	3	US-08-555-568B-23
8	1531	100.0	688	4	US-09-519-223-23
9	1531	100.0	688	4	US-09-927-180-23
10	1524	99.5	819	4	US-09-949-016-10948
11	1471	96.1	752	1	US-08-281-193-2
12	1471	96.1	752	1	US-08-422-106-2
13	1471	96.1	752	2	US-08-735-716-2
14	1471	96.1	752	2	US-08-555-568B-2
15	1471	96.1	752	3	US-09-519-223-2
16	1471	96.1	752	4	US-09-927-180-2
17	1471	96.1	752	5	PCT-US95-08069-2
18	736	48.1	896	4	US-09-270-767-46130
19	610	39.8	545	4	US-09-270-767-61684
20	371	24.2	143	4	US-09-270-767-33298
21	177	11.6	410	4	US-09-755-630B-290
22	177	11.6	410	4	US-09-755-630B-292
23	177	11.6	410	4	US-09-755-274-10
24	177	11.6	410	4	US-09-755-274-12
25	175	11.4	337	4	US-09-755-630B-293
26	175	11.4	337	4	US-09-755-274-13
27	175	11.4	410	2	US-08-449-986-2

28	175	11.4	410	2	US-08-756-855-2	Sequence 2, Appli
29	175	11.4	410	4	US-09-755-630B-288	Sequence 288, App
30	175	11.4	410	4	US-09-755-630B-291	Sequence 291, App
31	175	11.4	410	4	US-09-755-274-8	Sequence 8, Appli
32	175	11.4	410	4	US-09-755-274-11	Sequence 11, Appl
33	175	11.4	508	4	US-09-755-630B-289	Sequence 289, App
34	175	11.4	508	4	US-09-755-274-9	Sequence 9, Appli
35	142.5	9.3	383	1	US-07-936-163-4	Sequence 4, Appli
36	140	9.1	381	1	US-07-936-163-3	Sequence 3, Appli
37	140	9.1	386	4	US-09-755-630B-278	Sequence 278, App
38	140	9.1	386	4	US-09-755-274-5	Sequence 5, Appli
39	139	9.1	366	4	US-09-755-630B-263	Sequence 263, App
40	139	9.1	366	4	US-09-755-274-29	Sequence 29, Appl
41	138	9.0	367	4	US-09-755-630B-7	Sequence 7, Appli
42	138	9.0	367	4	US-09-755-274-41	Sequence 41, Appl
43	138	9.0	386	4	US-09-755-630B-2	Sequence 2, Appli
44	138	9.0	386	4	US-09-755-630B-265	Sequence 265, App
45	138	9.0	386	4	US-09-755-630B-286	Sequence 286, App

ALIGNMENTS

RESULT 1
US-08-555-568B-19
; Sequence 19, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-19

Query Match 100.0%; Score 1531; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 9.1e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LQDLHISRARPAFILGSMRDEKTRHLLCLDGGVKGIIIIQLLIAIEKASGVATKD	60
Db	1	LQDLHISRARPAFILGSMRDEKTRHLLCLDGGVKGIIIIQLLIAIEKASGVATKD	60
QY	61	LFDWVAGTGTGGILALAILHKSMAVMGMGMKDEVRGSRPYSGPLEFLKRFGE	120
Db	61	LFDWVAGTGTGGILALAILHKSMAVMGMGMKDEVRGSRPYSGPLEFLKRFGE	120

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Db      380 KMWQAIRASSAAGGYFAEYALGNLDLHQDGGLLNNPSALAMHECKCLWPDV----- 430
Qy      235 KKLIVVSLGTGR 247
Db      431 -PLECIVSLGTGR 442
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RESULT 15
US-10-786-505-18
; Sequence 18, Application US/10786505
; Publication No. US20050003388A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, RICHARD W.
; APPLICANT: DAVID J. MANCUSO
; TITLE OF INVENTION: CALCIUM INDEPENDENT PHOSPHOLIPASE A2V POLYNUCLEOTIDES
; TITLE OF INVENTION: AND POLYPEPTIDES AND METHODS THEREFOR
; FILE REFERENCE: 15060-58
; CURRENT APPLICATION NUMBER: US/10/786,505
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: 09/168,623
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-786-505-18
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Query Match      13.8%; Score 211.5; DB 16; Length 661;
Best Local Similarity 28.5%; Pred. No. 8.3e-13;
Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;

Qy      16 ILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILA 75
Db      309 LIGYDVPVKGRIILSIDGGTGRGVVALQTLRKLVELTQKPVHQLFDYICGVSTGAILA 368

Qy      76 LAI-LHKSMAVMRGMYFRMKDVER-----GSRPVESGPLEEFLKREFGEHT 122
Db      369 FMLGLFHMPLDECEELYRLKLGSDVFSQNVIVGTVMKWSHAFYDSQTWENILKDRMGSA 428

Qy      123 KMTDVRK---PKVMLTGTLSDRQ-PAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQ 178
Db      429 MIETARNPTCPKVAAVSTIVNRGITPKAFVFRNYG-----HFPGINSHY-----LGGCOY 478

Qy      179 LVWRAARSSGAAPTYFRP-----NGRFLDGGLLANNPTLDAMTEIHEYNQOOLIRKGOANKV 234
Db      479 KMWQAIRASSAAGGYFAEYALGNLDLHQDGGLLNNPSALAMHECKCLWPDV----- 529

Qy      235 KKLIVVSLGTGR 247
Db      530 -PLECIVSLGTGR 541
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Search completed: May 26, 2005, 14:51:04
Job time : 41.8117 secs


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; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-4998

Query Match      17.0%; Score 261; DB 15; Length 468;
Best Local Similarity 29.8%; Pred. No. 3.1e-18;
Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

QY 16 ILGSMRDEKRTDH-LLCLDGGGVKGLIIQLLIAIEKASGVATKDLFWVAGTSTGGIL 74
DB 180 VLASEKKQWKEPVRVLLALDGGGIRAVITQMLIHIDYLLGGKLVKELDDIAGTSCGVI 239

QY 75 ALAI-LHKSMAVMRGMYFRMKDEVF-RGSR---PVESGPLEBEFLKREF--GEHTKMTDV 127
DB 240 TLLSTNNRINBETRLKLLDMRDVIRGADKAVPKYSSNGMEYIARHVTTWEDSKWSSI 299

QY 128 RKPVKMLTGTLSDRQPAELHFRNY--DAPETVREP-RFNQNVNLRPPAQPSDQLVWRAA 184
DB 300 KRHRIVTVADTWMVPQLLLFRSYRPEMPEACEHYKF-----LDPTKVELWKTL 350

QY 185 RSGGAAPTFRNRGFLDGGLLANNPTLDMATIEHYNQDLIRKQANKV-----K 236
DB 351 RCTTAAPYFFESPNGLSDGLIANNPALISDFLTNK--LEKSPAKSSSERENRGWVK 408

QY 237 LSIIVSLGTGRSPQVPVTCVDV 258
DB 409 IGVISLGTGVPTXKIDGIDL 430

RESULT 10
US-10-437-963-169583
; Sequence 169583, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169583
; LENGTH: 1254
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67990C.1.pap
US-10-437-963-169583

Query Match      15.3%; Score 235; DB 16; Length 1254;
Best Local Similarity 25.9%; Pred. No. 7.2e-15;
Matches 89; Conservative 48; Mismatches 101; Indels 106; Gaps 15;

QY 1 IQDLM-----HISRARKPAP-ILGSMRDEKRTDH-----HLCLDGGGVKGL 41
DB 487 LRDLRLTLTSQEKRVSKAAARALAILGENENLRRAIRGPVAKGLRLILSDGGGKGL 546
QY 42 IIIQLLIAIEKASGVATKDLFWVAGTSTGGILALAI-LHKSMAVMRGMYFRM----- 94

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DB 547 ATVQILKQIEQGTGRIHEMFDLICTSTGGLMALGALGQKMTLDOCEBIYTKGLKLVFA 606
QY 95 ----KDE-----VFRSGRPYESGPLBEFLKR-----EFGHTKMT 125
DB 607 EPAPKDEAATWKEKIDQLFKSSQSFRVVVHGSK-HSADQFERLLKEMCADEGDGLLIES 665
QY 126 DVRK-PKVMLTGTLSDRQPAELHFRNYDAPETVRE-----PRFNQNVN 168
DB 666 AVKGIPKFAVSTLVSVMPAQPIFRNYQYPTGTVEVSSVMTESPISGAGTIVSGAPVG 725
QY 169 LRP-----PAQP-----SDQLVWRAARSSGAAPTY----FRPN-GRFLDGGGL 725
DB 726 IKPINTVGTAVSGAPVGIKRGAFMGSKHRIWEAIRASSAAPYLDDFDDVNRWQDGAI 785
QY 206 LANNPTLDMATIEHYNQDLIRKQANKVLSIVVSLGTGRSP 249
DB 786 VANNPTIFAIRAQLLWPD-----TRIDCLVSGCGSVP 819

RESULT 11
US-10-421-654-66
; Sequence 66, Application US/10421654
; Publication No. US20040005604A1
; GENERAL INFORMATION:
; APPLICANT: Gramatikova, Svetlana
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Lam, David E.
; APPLICANT: Barton, Nelson R.
; TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 09010-094001
; CURRENT APPLICATION NUMBER: US/10/421,654
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US 60/374,313
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-421-654-66

Query Match      15.3%; Score 234; DB 15; Length 387;
Best Local Similarity 27.8%; Pred. No. 1.6e-15;
Matches 89; Conservative 39; Mismatches 112; Indels 80; Gaps 13;

QY 30 LLCLDGGGVKGLIIQLLIAIE-----KASGVATKDLFWVAGTSTGGILALAILHS 81
DB 17 ILACDGGGILGLMSVEILAKIEADRLTKGDKQNFVLADYDFVCGTGTGAIAACISSG 76
QY 82 KSMAYMRGMYFRMKDEVF-----RGSRPYSGPLEEFLKREFGHEHTKMTDVRKPKVML 134
DB 77 MSMAKIRQFYLDGSKGMFDEKASLLKRLQYSYDDEFLARQIRAAFDQLKETDAKLSAHL 136
QY 135 TGTLSDRQPAELHFRNY--DAPETVRE---PRFN---QNVNLRPPAQPSDQLVWRAAR 185
DB 137 KTLI-----MMVMRNHSTDSFPVSNPNYAKYNNIARKDCNCLNP-----LWQLVR 182
QY 186 SSGAAPTFRP-----NGRFLDGGLLA-NNPTLDMATIEHYNQDLIRKQQA 231
DB 183 ASTAAPTVPFPPPEVITFADGTPEEYNFIFVDGGVTTNNPAYLAFLMATKPYALNWPPTS 242
QY 232 NKVKKLSIVSLGTGRSPQV-PVTCVD-----VFRPSNPWEAKTVFGA-- 274
DB 243 NQL-----LIVSGTGSAAANVRNLDVDDMNLIHFAKNIPSALMNAASAGWDMTCRVLGEC 298
QY 275 -----KELGQWVDDCCDT 287
DB 299 RHGGMLDREFGDMVMPASRD 318

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QY 1 LQDLMHISRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 397 LQDLMHISRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
Db 457 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGE 516
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLPFNYPADPVTREPRNQNVNLRPPAQPDSQLV 180
Db 517 HTKMTDVRKPKVMLTGTLSDRQPAELHLPFNYPADPVTREPRNQNVNLRPPAQPDSQLV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
Db 577 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 292
Db 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 688

RESULT 4
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 99.5%; Score 1524; DB 15; Length 667;
Best Local Similarity 100.0%; Pred. No. 5.9e-151;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 312 LQDLMHISRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 371
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
Db 372 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGE 431
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLPFNYPADPVTREPRNQNVNLRPPAQPDSQLV 180
Db 432 HTKMTDVRKPKVMLTGTLSDRQPAELHLPFNYPADPVTREPRNQNVNLRPPAQPDSQLV 491
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
Db 492 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 551
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
Db 552 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 602

RESULT 5
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match 96.1%; Score 1471; DB 9; Length 752;
Best Local Similarity 95.2%; Pred. No. 2.7e-145;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
QY 1 LQDLMHISRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 397 LQDLMHISRARKPAFILGSMRDEKTRHDHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
Db 457 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGE 516
QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLPFNYPADPVTREPRNQNVNLRPPAQPDSQLV 180
Db 517 HTKMTDVRKPKVMLTGTLSDRQPAELHLPFNYPADPVTREPRNQNVNLRPPAQPDSQLV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
Db 577 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 291
Db 637 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 6
US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B

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; LENGTH: 292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19
Query Match 100.0%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRAKPAFLGSMRDEKTRTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 60
Db 1 LQDLMHISRAKPAFLGSMRDEKTRTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWAGTSTGGILALAILHKSMAVMGMFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120
Db 61 LFDWAGTSTGGILALAILHKSMAVMGMFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
QY 181 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
Db 181 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
QY 241 VSLGTGRSPQVPTVCDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 292
Db 241 VSLGTGRSPQVPTVCDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 292
RESULT 2
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-23
Query Match 100.0%; Score 1531; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRAKPAFLGSMRDEKTRTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 60
Db 1 LQDLMHISRAKPAFLGSMRDEKTRTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKD 60
QY 61 LFDWAGTSTGGILALAILHKSMAVMGMFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120
Db 61 LFDWAGTSTGGILALAILHKSMAVMGMFRMKDEVFGRSGRPYSGPLEEFLKREFGE 120
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
Db 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
QY 181 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
Db 181 WRAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
QY 241 VSLGTGRSPQVPTVCDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 292
Db 241 VSLGTGRSPQVPTVCDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPPGRP 292
RESULT 3
US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23
Query Match 100.0%; Score 1531; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 39.8117 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLMHISRARPAFILGSM.....GAKELGKMVVDCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA:*

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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1531	100.0	292	9 US-09-927-180-19	Sequence 19, Appl
2	1531	100.0	687	9 US-09-927-180-21	Sequence 21, Appl
3	1531	100.0	688	9 US-09-927-180-23	Sequence 23, Appl
4	1524	99.5	667	15 US-10-108-260A-3778	Sequence 3778, Ap
5	1471	96.1	752	9 US-09-927-180-2	Sequence 2, Appli
6	456.5	29.8	1071	15 US-10-369-493-6865	Sequence 6865, Ap
7	419	27.4	1023	15 US-10-369-493-6689	Sequence 6689, Ap
8	419	27.4	1023	15 US-10-369-493-6690	Sequence 6690, Ap
9	261	17.0	468	15 US-10-369-493-4998	Sequence 4998, Ap
10	235	15.3	1254	16 US-10-431-963-169583	Sequence 169583,
11	234	15.3	387	15 US-10-421-654-66	Sequence 66, Appl
12	234	15.3	387	17 US-10-796-907-66	Sequence 66, Appl
13	211.5	13.8	370	9 US-09-925-300-1483	Sequence 1483, Ap

Sequence 21, Appl
Sequence 18, Appl
Sequence 15, Appl
Sequence 1, Appl
Sequence 100, App
Sequence 132, App
Sequence 616, App
Sequence 259117,
Sequence 615, App
Sequence 258423,
Sequence 177823,
Sequence 18, Appl
Sequence 18, Appl
Sequence 290, App
Sequence 292, App
Sequence 39447, A
Sequence 39376, A
Sequence 47375, A
Sequence 57061, A
Sequence 138254,
Sequence 72032, A
Sequence 72035, A
Sequence 65072, A
Sequence 293, App
Sequence 288, App
Sequence 291, App
Sequence 39450, A
Sequence 47374, A
Sequence 289, App
Sequence 129647,
Sequence 242149,

211.5 13.8 562 16 US-10-786-505-21
15 211.5 13.8 661 16 US-10-786-505-18
16 211.5 13.8 682 16 US-10-786-505-15
17 211.5 13.8 782 16 US-10-786-505-1
18 208.5 13.6 350 15 US-10-421-654-100
19 208.5 13.6 350 17 US-10-796-907-100
20 207.5 13.6 308 17 US-10-796-907-132
21 204.5 13.4 577 15 US-10-310-154-616
22 201 13.1 315 15 US-10-424-599-259117
23 201 13.1 382 15 US-10-310-154-615
24 195.5 12.8 382 15 US-10-424-599-258423
25 193.5 12.6 387 16 US-10-437-963-177823
26 190 12.4 378 15 US-10-421-654-18
27 190 12.4 378 17 US-10-796-907-18
28 177 11.6 410 10 US-09-755-630A-290
29 177 11.6 410 10 US-09-755-630A-292
30 177 11.6 434 15 US-10-425-114-39447
31 177 11.6 437 15 US-10-425-114-39376
32 177 11.6 439 15 US-10-425-114-47375
33 177 11.6 441 15 US-10-425-114-57061
34 177 11.6 442 16 US-10-437-963-138254
35 176 11.5 438 15 US-10-425-114-72032
36 176 11.5 438 15 US-10-425-114-72035
37 176 11.5 448 15 US-10-425-114-65072
38 175 11.4 337 10 US-09-755-630A-293
39 175 11.4 410 10 US-09-755-630A-288
40 175 11.4 410 10 US-09-755-630A-291
41 175 11.4 436 15 US-10-425-114-39450
42 175 11.4 436 15 US-10-425-114-47374
43 175 11.4 508 10 US-09-755-630A-289
44 174.5 11.4 405 16 US-10-437-963-129647
45 174 11.4 463 15 US-10-424-599-242149

ALIGNMENTS

RESULT 1

US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;

Sequence 752 AA;

PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX Claim 7; SEQ ID NO 700; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 806 AA;
Query Match 99.5%; Score 1524; DB 8; Length 806;
Best Local Similarity 100.0%; Pred. No. 8.7e-162;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LODLMIHSRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 451 LODLMIHSRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 510
QY 61 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 120
Db 511 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 570
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLPRNYDAPETVREPRNQNVNLRPPAQPSDQLV 180
Db 571 HTKMTDVRKPKVMTGTLSDRQPAELHLPRNYDAPETVREPRNQNVNLRPPAQPSDQLV 630
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 240
Db 631 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGQANKVKLSIV 690
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGR 291
Db 691 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCCCTDPDGR 741
RESULT 11
ABM84355
ID ABM84355 standard; protein; 810 AA.
XX
AC ABM84355;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatury S, Shi X, Suarez CU;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43007.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 810 AA;
Query Match 97.9%; Score 1499; DB 8; Length 810;
Best Local Similarity 90.7%; Pred. No. 5.7e-159;
Matches 291; Conservative 0; Mismatches 0; Indels 30; Gaps 1;
QY 1 LODLMIHSRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
Db 425 LODLMIHSRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 484
QY 61 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 120
Db 485 LFDWAGTGTGGILALAILHLSKSMAYMRGMVFRMKDEVERGSRPYSGPLEEFLKREFGE 544
QY 121 HTKMTDVRKPK-----VMTGTLSDRQPAELHLFR 150
Db 545 HTKMTDVRKPKLDQSDTTPALPERACFAGMVRGEAHLSTRTEVMTGTLSDRQPAELHLFR 604
QY 151 NYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGLLANNP 210
Db 605 NYDAPETVREPRNQNVNLRPPAQPSDQLVWRAARSSGAAPTYFRPNRFLDGLLANNP 664
QY 211 TLDMATEIHEYNDLIRKGQANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNPWELAKT 270
Db 665 TLDMATEIHEYNDLIRKGQANKVKLSIVVSLGTRSPQVPVTCVDVFRPSNPWELAKT 724
QY 271 VFGAKELGKMVVDCCCTDPDGR 291
Db 725 VFGAKELGKMVVDCCCTDPDGR 745
RESULT 12
ABM84354
ID ABM84354 standard; protein; 810 AA.
XX
AC ABM84354;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.

CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
 CC also relates to the assessment of the effects of exogenous compounds on
 CC the expression of nucleic acids and LipAms. The invention provides
 CC expression vectors, host cells, antibodies, agonists and antagonists,
 CC transgenic organisms, and arrays and microarrays of the polynucleotides.
 XX
 XX Sequence 784 AA;

Query Match 99.5%; Score 1524; DB 7; Length 784;
 Best Local Similarity 100.0%; Pred. No. 8.3e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIQLLIAIERKASGVATKD 60
 Db LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIQLLIAIERKASGVATKD 488
 QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFGRSPYSGPLEEFLKREFGE 120
 Db LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFGRSPYSGPLEEFLKREFGE 548
 QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
 Db HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 608
 QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
 Db WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 668
 QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 291
 Db VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 719

RESULT 9
 AAE25968
 ID AAE25968 standard; protein; 806 AA.
 XX
 AC AAE25968;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human PLA2 group VI (Ca2+-independent) protein.
 XX
 KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KW antisense therapy; PLA2 protein.
 XX
 OS Homo sapiens.
 XX
 PN US6410325-B1.
 XX
 PD 25-JUN-2002.
 XX
 PF 09-MAY-2001; 2001US-00851896.
 XX
 PR 09-MAY-2001; 2001US-00851896.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Freier SM, Watt RT;
 XX
 DR WPI; 2002-616513/66.
 DR N-PSDB; AAD42941.
 XX

Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.
 XX
 PS Disclosure; Col 109-116; 72pp; English.
 XX
 CC The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,

CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein
 XX
 XX Sequence 806 AA;

Query Match 99.5%; Score 1524; DB 5; Length 806;
 Best Local Similarity 100.0%; Pred. No. 8.7e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIQLLIAIERKASGVATKD 60
 Db LODLHHSRARKPAFTLGSMDKRTDHLCLDGGVKGGLIIQLLIAIERKASGVATKD 510
 QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFGRSPYSGPLEEFLKREFGE 120
 Db LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFGRSPYSGPLEEFLKREFGE 570
 QY 121 HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 180
 Db HTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQIV 630
 QY 181 WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
 Db WRAARSSGAAPTYFRPNRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 690
 QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 291
 Db VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR 741

RESULT 10
 ADO19776
 ID ADO19776 standard; protein; 806 AA.
 XX
 AC ADO19776;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #350.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI; 2004-420067/39.
 DR N-PSDB; ADO19775.
 XX

Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,

Db	577	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	636
QY	241	VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP	292
Db	637	VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGRP	688
RESULT 7			
ADM05093	ID	ADM05093 standard; protein; 667 AA.	
XX	AC	ADM05093;	
XX	DT	20-MAY-2004 (first entry)	
XX	DE	Human protein of the invention SEQ ID NO:3778.	
XX	KW	human; gene therapy; diagnostic marker; pharmaceutical.	
XX	OS	Homo sapiens.	
XX	PN	EP1347046-A1.	
XX	PD	24-SEP-2003.	
XX	PF	12-APR-2002; 2002EP-00008400.	
XX	PR	22-MAR-2002; 2002JP-00137785.	
XX	PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
XX	PI	Isogai T, Sugiyama T, Otsuka T, Wakamatsu A, Sato H, Ishii S;	
XX	PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;	
XX	PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;	
XX	WPI	2003-723558/69.	
XX	N-PSDB	ADM02650.	
XX	PT	New polynucleotides and polypeptides are useful in gene therapy, for	
XX	PT	developing a diagnostic marker or medicines for regulating their	
XX	PT	expression and activity, or as a target of gene therapy.	
XX	PS	Claim 1; SEQ ID NO 3778; 305pp; English.	
XX	CC	The invention relates to a novel human polynucleotide and the encoded	
XX	CC	polypeptide. A polynucleotide of the invention may have a use in gene	
XX	CC	therapy. An oligonucleotide of the invention ADM06773 is useful	
XX	CC	as a primer for synthesizing the polynucleotide or as a probe for	
XX	CC	detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are	
XX	CC	useful in gene therapy, for developing a diagnostic marker or medicines	
XX	CC	for regulating their expression and activity, or as a target of gene	
XX	CC	therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides	
XX	CC	are useful as pharmaceutical agents. The present sequence represents a	
XX	CC	protein sequence of the invention.	
XX	SQ	Sequence 667 AA;	
Query Match			
Best Local Similarity 99.5%; Score 1524; DB 7; Length 667;			
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	LQDLMHISRKAPAFILGSMRDEKRTDHLCLDGGVKGGLIIQLLIAIEKASGVATKD	60
Db	312	LQDLMHISRKAPAFILGSMRDEKRTDHLCLDGGVKGGLIIQLLIAIEKASGVATKD	371
QY	61	LFDWVAGTGTGILALAILHKSMAWYMRGMVFMRKDEVFRGSRPYESGPLEBFLKEEFG	120
Db	372	LFDWVAGTGTGILALAILHKSMAWYMRGMVFMRKDEVFRGSRPYESGPLEBFLKEEFG	431
QY	121	HTKMTDVRKPKVMTLTLSRQPAELHLPFRNDAPETVREPRFNQNNLRPPAQPSDQLV	180
Db	432	HTKMTDVRKPKVMTLTLSRQPAELHLPFRNDAPETVREPRFNQNNLRPPAQPSDQLV	491
QY	181	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	240
Db	492	WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKGOANKVKLSIV	551
QY	241	VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	291
Db	552	VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDDCCTDPDGR	602
RESULT 8			
ADD93407	ID	ADD93407 standard; protein; 784 AA.	
XX	AC	ADD93407;	
XX	DT	29-JAN-2004 (first entry)	
XX	DE	Human lipid-associated molecule LIPAM-14 polypeptide.	
XX	KW	Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;	
XX	KW	antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;	
XX	KW	antiinflammatory; thymimetic; antiallergic; cerebroprotective;	
XX	KW	gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;	
XX	KW	antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;	
XX	KW	virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;	
XX	OS	Homo sapiens.	
XX	PN	WO2003093081-A2.	
XX	PD	09-OCT-2003.	
XX	PF	27-MAR-2003; 2003WO-US009755.	
XX	PR	29-MAR-2002; 2002US-0368722P.	
XX	PR	03-MAY-2002; 2002US-0377576P.	
XX	PR	05-JUL-2002; 2002US-0393934P.	
XX	PR	27-SEP-2002; 2002US-0414269P.	
XX	PA	(INCY-) INCYTE CORP.	
XX	PI	Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;	
XX	PI	Baughn MR, Lee EA, Griffin JA, Kable AE, Elliott VS, Chang H;	
XX	PI	Lee S, Ramkumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;	
XX	PI	Jackson AA;	
XX	WPI	2003-788347/74.	
XX	N-PSDB	ADD93426.	
XX	PT	New LIPAM polypeptides, useful for diagnosing, preventing, and treating	
XX	PT	disorders associated with abnormal expression or activity of LIPAM, e.g.	
XX	PT	neuromuscular, immunological, cardiovascular disorders, cancer and/or	
XX	PT	infections.	
XX	PS	Claim 69; Page 206-207; 238pp; English.	
XX	CC	The present sequence is the protein sequence of human lipid-associated	
XX	CC	molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows	
XX	CC	homology to human Ca2+-independent phospholipase A2 short isoform. This	
XX	CC	is one of 19 LIPAM polypeptides of the invention. The invention relates	
XX	CC	to these novel LIPAMs and the nucleic acids encoding them, and to the use	
XX	CC	of nucleic acids and proteins in the diagnosis, treatment and prevention	
XX	CC	of disorders associated with abnormal expression or activity of LIPAM	
XX	CC	such as neurodegenerative disorders (e.g. Parkinson's disease,	
XX	CC	Alzheimer's disease), muscular disorders (e.g. diabetes, Grave's disease), cancers	
XX	CC	(e.g. leukaemia, cervical or breast cancers), immunological disorders	
CC	CC	(e.g. scleroderma, systemic lupus erythematosus, allergies),	
CC	CC	gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.	
CC	CC	Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,	
CC	CC	parasitic, protozoal, helminthic), cardiovascular disorders (e.g.	

inflammation; inhibitor; antiinflammatory.
Homo sapiens.
WO9717448-A2.
15-MAY-1997.
07-NOV-1996; 96WO-US017794.
08-NOV-1995; 95US-00555568.
(GEMY) GENETICS INST INC.
Jones S, Tang J;
WPI; 1997-281037/25.
N-PSDB; AAT68826.
Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.
Claim 12; Page 54-56; 74pp; English.
A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839-44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade
Sequence 688 AA;
Query Match 100.0%; Score 1531; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LQDLMHISRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 456
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120
DB 457 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 516
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180
DB 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 636
QY 241 VSLGTRSPQVPVTCVDVFRPNPNWELAKTVFGAKELGMVVDCCDTPDGRP 292
DB 637 VSLGTRSPQVPVTCVDVFRPNPNWELAKTVFGAKELGMVVDCCDTPDGRP 688
RESULT 6
AB82232
ID AB82232 standard; protein; 688 AA.
XX AC AB82232;
XX AC AB82232;
DT 08-JAN-2003 (first entry)
XX

Human cPLA2/B splice variant (clone 19b).
Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
antiasthmatic; human.
Homo sapiens.
US2002106364-A1.
08-AUG-2002.
09-AUG-2001; 2001US-00927180.
27-JUL-1994; 94US-00281193.
14-APR-1995; 95US-00422106.
14-APR-1995; 95US-00422420.
26-JUN-1995; 95WO-US008069.
08-NOV-1995; 95US-00555568.
09-SEP-1998; 98US-00149988.
06-MAR-2000; 2000US-00519223.
(GEMY) GENETICS INST INC.
Jones S, Tang J;
WPI; 2002-739923/80.
N-PSDB; ABV73011.
Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
Claim 6; Page 28-30; 41pp; English.
The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme longer splice variant (clone 19b)
Sequence 688 AA;
Query Match 100.0%; Score 1531; DB 5; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 397 LQDLMHISRARKPAFILGSMRDEKTRTHLLCLDGGGVKGLIIQLLIAIEKASGVATKD 456
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 120
DB 457 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEFLKREFGE 516
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 180
DB 517 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX mammalian subject.
PS Claim 12; Page 49-51; 74pp; English.
XX
XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
CC characterized by activity in the absence of calcium, by activity in a
CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
CC lack of stimulation by ATP, and by including in its sequence at least one
CC of the amino acid sequences given in AAW17839- 44). It is an
CC alternatively spliced variant of another isolated polypeptide (AAW17845)
CC and is encoded by an isolated cDNA (AAW68825). Other sPLA2/B enzymes
CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
CC thought to be involved in the release of arachidonic acid in specific
CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
CC drugs which inhibit the arachidonic acid cascade
XX
SQ Sequence 687 AA;
Query Match 100.0%; Score 1531; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARPAPFILGSMRDEKTRHDHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 60
Db 396 LQDLMHISRARPAPFILGSMRDEKTRHDHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 455
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEFLKREFGE 120
Db 456 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEFLKREFGE 515
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
Db 516 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575
QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
Db 576 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 635
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
Db 636 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 687
RESULT 4
ABB82231
XX ABB82231 standard; protein; 687 AA.
XX
XX ABB82231;
XX
XX
DT 08-JAN-2003 (first entry)
XX Human cPLA2/B splice variant (clone 19a).
DE
DE Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
KW antiasthmatic; human.
XX
XX Homo sapiens.
XX
XX US2002106364-A1.
PN
XX
PD 08-AUG-2002.
XX
XX 09-AUG-2001; 2001US-00927180.
PF
XX
PR 27-JUL-1994; 94US-00281193.
PR 14-APR-1995; 95US-00422106.
PR 14-APR-1995; 95US-00422420.
PR 26-JUN-1995; 95WO-US008069.
PR 08-NOV-1995; 95US-00555568.

PR 09-SEP-1998; 98US-00149988.
PR 06-MAR-2000; 2000US-00519223.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jones S, Tang J;
PI
DR WPI; 2002-739923/80.
DR N-PSDB; ABV73010.
XX
XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
XX
XX Claim 6; Page 23-25; 41pp; English.
CC The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
CC 19a)
XX
SQ Sequence 687 AA;
Query Match 100.0%; Score 1531; DB 5; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-162;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQDLMHISRARPAPFILGSMRDEKTRHDHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 60
Db 396 LQDLMHISRARPAPFILGSMRDEKTRHDHLLCLDGGGVKGLIIIIQLLIAIEKASGVATKD 455
QY 61 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEFLKREFGE 120
Db 456 LFDWAGTSTGGILALAILHKSMAVMRGMYFRMKDEVERGSRPYESGPLEFLKREFGE 515
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
Db 516 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 575
QY 181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
Db 576 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 635
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
Db 636 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 687
RESULT 5
AAW17848
ID AAW17848 standard; protein; 688 AA.
XX
XX AAW17848;
XX
XX
DT 07-AUG-1997 (first entry)
XX
DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
XX
KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

XX	Sequence 292 AA;	CC	characterized by activity in the absence of calcium and has a molecular weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified calcium independent phospholipase enzyme is useful for identifying an inhibitor of phospholipase activity which involves combining (I), phospholipid and candidate inhibitor compound, and observing whether the enzyme cleaves the phospholipid and releases fatty acid from it. A pharmaceutical composition (PC) comprising a therapeutically effective amount of the inhibitor is useful for reducing inflammation and for treating inflammatory conditions including rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease and other diseases mediated by increased levels of prostaglandins, leukotriene or platelet activating factor. A composition comprising an antibody which binds to (I) is useful as research and diagnostic tool, and is also useful in the study of phospholipase A2 activity and inflammatory conditions. The present sequence represents a human cPLA2/B enzyme (clone 19b)
SQ		XX	
Query Match	100.0%; Score 1531; DB 2; Length 292;	CC	
Best Local Similarity	100.0%; Pred. No. 2.9e-163;	CC	
Matches 292; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	CC	
QY	1 LODLWHISARKAPAFILGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60	CC	
DB	1 LODLWHISARKAPAFILGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60	CC	
QY	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120	CC	
DB	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120	CC	
QY	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180	CC	
DB	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180	CC	
QY	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240	CC	
DB	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240	CC	
QY	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDPDGRP 292	CC	
DB	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDPDGRP 292	CC	
RESULT 2		XX	
ABB82230		XX	
ID	ABB82230 standard; protein; 292 AA.	XX	
AC	ABB82230;	XX	
XX		XX	
DT	08-JAN-2003 (first entry)	XX	
DE	Calcium independent phospholipase A2/B (cPLA2/B) (clone 19b).	XX	
XX		XX	
KW	Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme; antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic; antiasthmatic; human.	XX	
OS	Homo sapiens.	XX	
XX		XX	
PN	US2002106364-A1.	XX	
PD	08-AUG-2002.	XX	
PF	09-AUG-2001; 2001US-00927180.	XX	
PR	27-JUL-1994; 94US-00281193.	XX	
PR	14-APR-1995; 95US-00422106.	XX	
PR	14-APR-1995; 95US-00422420.	XX	
PR	26-JUN-1995; 95WO-US008069.	XX	
PR	08-NOV-1995; 95US-00555568.	XX	
PR	09-SEP-1998; 98US-00149588.	XX	
PR	06-MAR-2000; 2000US-00519223.	XX	
PA	(GEMY) GENETICS INST INC.	XX	
PI	Jones S, Tang J;	XX	
XX		XX	
DR	WPI; 2002-739923/80.	XX	
DR	N-PSDB; ABV73009.	XX	
PT	Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.	XX	
PS	Claim 6; Page 21-22; 4lpp; English.	XX	
CC	The invention relates to a purified mammalian calcium independent cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is	XX	
CC		XX	
Query Match	100.0%; Score 1531; DB 5; Length 292;	CC	
Best Local Similarity	100.0%; Pred. No. 2.9e-163;	CC	
Matches 292; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	CC	
QY	1 LODLWHISARKAPAFILGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60	CC	
DB	1 LODLWHISARKAPAFILGMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60	CC	
QY	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120	CC	
DB	61 LFDWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVFRGSRPYESGPLEBFLKREFGE 120	CC	
QY	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180	CC	
DB	121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180	CC	
QY	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240	CC	
DB	181 WRAARSSGAAPTYFRPNGRFLDGLLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240	CC	
QY	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDPDGRP 292	CC	
DB	241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGMVVDCCCTDPDGRP 292	CC	
RESULT 3		XX	
AAW17847		XX	
ID	AAW17847 standard; protein; 687 AA.	XX	
AC	AAW17847;	XX	
XX		XX	
DT	07-AUG-1997 (first entry)	XX	
DE	Cytosolic phospholipase A2/B (alternatively spliced clone 19a).	XX	
XX		XX	
KW	Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory.	XX	
XX		XX	
OS	Homo sapiens.	XX	
XX		XX	
PN	WO9717448-A2.	XX	
PD	15-MAY-1997.	XX	
XX		XX	
PF	07-NOV-1996; 96WO-US017794.	XX	
XX		XX	
PR	08-NOV-1995; 95US-00555568.	XX	
XX	(GEMY) GENETICS INST INC.	XX	
PI	Jones S, Tang J;	XX	
XX		XX	
DR	WPI; 1997-281037/25.	XX	
DR	N-PSDB; AAT68825.	XX	

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 37.6866 Seconds
(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LQDLMHISRAKPAFILGSM.....GAKELGKMVDDCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1531	100.0	292	2	AAW17846	Cytosolic
2	1531	100.0	292	5	ABB82230	Calcium i
3	1531	100.0	687	2	AAW17847	Cytosolic
4	1531	100.0	687	5	ABB82231	Human cpl
5	1531	100.0	688	2	AAW17848	Cytosolic
6	1531	100.0	688	5	ABB82232	Human cpl
7	1524	99.5	667	7	ADMO5093	Human pro
8	1524	99.5	784	7	ADQ93407	Human lip
9	1524	99.5	806	5	AAE25968	Human PLA
10	1524	99.5	806	8	ADQ19776	Human PRO
11	1499	97.9	810	8	ABM84355	Human dia
12	1499	97.9	810	8	ABM84354	Human dia
13	1471	96.1	752	2	AAW17849	Calcium-i
14	1471	96.1	752	2	AAW17849	Calcium-i
15	1471	96.1	752	2	AAW17849	Calcium-i
16	1471	96.1	752	2	AAW17849	Calcium-i
17	1471	96.1	752	2	AAW17849	Calcium-i
18	1471	96.1	752	5	ABW81825	Chinese h
19	1454	95.0	751	7	ADDE60532	Rat Prote
20	1454	95.0	751	7	ADDE60532	Rat Prote
21	1454	95.0	751	7	ADDE60532	Rat Prote
22	1454	95.0	751	7	ADDE60536	Rat Prote
23	890	58.1	401	4	AAW17849	Human pro
24	736	48.1	877	4	ABW82231	Drosophil
25	456.5	29.8	1071	8	ADN24212	Bacterial

ALIGNMENTS

RESULT 1
AAW17846
ID AAW17846 standard; protein; 292 AA.
AC
XX AAW17846;
XX
XX
DT 07-AUG-1997 (first entry)
XX
DE Cytosolic phospholipase A2/B (clone 19b product).
XX
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW Inflammation; inhibitor; antiinflammatory.
XX
XX Homo sapiens.
XX
XX WO9717448-A2.
XX
XX
PD 15-MAY-1997.
XX
PF 07-NOV-1996; 96WO-US017794.
XX
PR 08-NOV-1995; 95US-00555568.
XX
(GEMY) GENETICS INST INC.
PA
XX Jones S, Tang J;
XX
XX WPI; 1997-281037/25.
DR N-PSDB; AAT68824.
XX
PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.
PT
XX
XX Claim 12; Page 46-47; 74pp; English.
XX
XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839- 44). It is encoded by partial cDNA clone 19b (AAT68824), derived from Burkitt's lymphoma Raji (ATCC CRL86) cells. Other PLA2/B enzymes (AAW17845, AAW17847-48) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Chertis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Curley J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D.L., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.H.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537558;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirska R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.S., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003550; RA050194.3; --
DR HSSP; Q60778; 10Y3.

DR FlyBase; FBgn0036053; CG6718.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 4.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT; 1.
KW ANK repeat.
SQ SEQUENCE 877 AA; 96862 MW; C9DC2CD6C282869B CRC64;

Query Match 48.1%; Score 736; DB 2; Length 877;
Best Local Similarity 50.9%; Pred. No. 3e-57;
Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMRDEKRTDHLCLDGGVGLIIIIQLLJALEKASGVATKDLDFVAGTSTGGILA 75
DB 539 IAAETGIDPYGRGLLCLDGGVGLVQLLEIEKLSRTPIIHMFOWIAGTSTGGILA 598
QY 76 LAILHKSMAVMRGMYFRMKDEVFGRSGPYESGPLEEFLEKREFGHTKMTDVRKPKVMT 135
DB 599 LALGCKTMRQCMGLYLAKKEQCFVSGRPNSEPPESILKDNLGFNVMTDKPKIMVT 658
QY 136 GTLSDRQPAELHLFNYDAPETVR---EPRFNQNVNLRPPAQPSPQLVWRAARSSGAAPT 192
DB 659 GVMADKEPVDLHLFRNYTSASDILGIVTPINNRI---PPQPSQLVWRAARAAAGAPS 715
QY 193 YFRPNRGFLDGLLANNPTLDAMTEIHEYNODLIRKQANKVKLSIVLSLGTGRSPQVP 252
DB 716 YFRAPRGFLDGLLANNPTLDAMTEIHEYNALRAGRESEAI PVSVNSLGTGHPVTE 775
QY 253 VTCVDVFRPSNPWEIAKTVFGAKELGKMWVDCCTDPDGR 291
DB 776 LKIDIVFRPESWDPAKLAYGLISTIGLLVDAQTCSDGR 814

RESULT 11
Q7KUD4
ID Q7KUD4 PRELIMINARY; PRT; 887 AA.
AC Q7KUD4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE CG6718-PB (CG6718-pc).
GN ORFNames=CG6718;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abrell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Chertis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Curley J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smillus D.E., Schnerk A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
DR EMBL; BC067375; AH67375.1; -.
DR HSSP; P20749; IKIB.
DR ZFIN; ZDB-GENE-040426-2079; zgc:77476.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKVRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PPS0088; ANK_REPEAT; 4.
DR PROSITE; PPS0297; ANK_REPEAT; 1.
DR ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 63.1%; Score 966.5; DB 2; Length 818;
Best Local Similarity 63.9%; Pred. No. 4.4e-78;
Matches 184; Conservative 31; Mismatches 48; Indels 25; Gaps 1;

QY 28 DHLCLDGGGVKGLIIIIQLIIAIEKASGVATKDLFDWAGTSTGGILALAILHLSKSMAY 87
DB 465 DRLLCLDGGIGKGLVLIQLIIAIEKEAGPIRELFDFVSTSTGGILALIVHGSWEYL 524

QY 88 RGMFYRMKDEVFRGSRPYSGPLEEFLKREFGHTKMTDVRKPKVMTLGTLSRQPAELH 147
DB 525 RCLYFRMKQVFKGSRPYSGPLEEFLKNEFGENTKMTDTPRVNMTVSLADRHFGELH 584

QY 148 LFRNYDAPETVREPRFNQNVNLRPPAQP-----SDOLVWR 182
DB 585 LFRNYDPPALQRPDPYKSTATQPLTVPGWEDDLLLLVGYTRPPKRRKVTDEOLVWR 644

QY 183 AARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVS 242
DB 645 AARSSGAAPTYFRPMGRFLDGGLLANNPTLDAMTEIHFQNKAKAQRDEVTRLGVVVS 704

QY 243 LGTGRSPQVPTCVDFVRPSNPWELAKTVFGAKELGKMVVDCTDPDG 290
DB 705 LGTGKPPQAVNSVDVFRPSNPTELAKTVFGVKELGKMLVDCCTDSGD 752

RESULT 9
Q8MR13 PRELIMINARY; PRT; 386 AA.
AC Q8MR13;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LD44515P.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Faragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV122192; NAM5704.1; -.
DR FlyBase; FBgn0036053; CG6718.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
SQ SEQUENCE 386 AA; 42693 MW; B32B7BCFC38541DD CRC64;

Query Match 48.1%; Score 736; DB 2; Length 386;
Best Local Similarity 50.9%; Pred. No. 1e-57;
Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMRDEKRTDHLCLDGGVKGGLIIIIQLIIAIEKASGVATKDLFDWAGTSTGGILA 75
DB 48 IAAEIGDKPYGRGLLCLDGGIGRLVQLVQMLEIEKLSRTPIIHPFDWIAGTSTGGILA 107

QY 76 LAILHSKSMAYMRGMVFRMKDEVFRGSRPYSGPLEEFLKREFGHTKMTDVRKPKVMTL 135
DB 108 LALCGCKTMRQCMGLYLRMKEQCFVRSRPNSEFFESILKDLNGEENWMTDIKHPKIMVT 167

QY 136 GTLSRQPAELHLFRNYDAPETVR---EPRFNQNVNLRPPAQPSDOLVWRAARSSGAAPT 192
DB 168 GVMADRKVPDLHLFRNYTSASDILGIVTVPINNRI---PPQPSQELVWRAARATGAAPS 224

QY 193 YFRPNGRFLDGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVP 252
DB 225 YFRAGRFLDGGLLANNPTLDAMTEIHEYNALRSAGREAIPIVSNVMSLGTGHIPVTE 284

QY 253 VTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPDGR 291
DB 285 LKXIDVFRPESWDTKLAYGISTIGNLLVDQATCSDGR 323

RESULT 10
Q9VT60 PRELIMINARY; PRT; 877 AA.
AC Q9VT60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6718-PA.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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[illegible]

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QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNNVLRPPAQPDSQVLV 180
Db 572 HTKMTDVKKPKVMTGTLSDRQPAELHLFRNYDAPEAVREPRCNQINLKPKPTQPADQLV 631
QY 181 WRAARSSGAAPTYFRPNGRFLDGLGGLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIV 240
Db 632 WRAARSSGAAPTYFRPNGRFLDGLGGLANNPTLDAMTEIHEYNODMIRKQGNKVKKLSIV 691
QY 241 VSLGTRSPQVPVTCVDVFRPNPWLAKTVFGAKELGKMWVDDCCTDPDGR 291
Db 692 VSLGTGKSPQVPVTCVDVFRPNPWLAKTVFGAKELGKMWVDDCCTDPDGR 742

RESULT 5
PA26 RAT
ID PA26 RAT STANDARD; PRT; 751 AA.
AC E97570;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.;
RT "Pancreatic islets express a Ca2+-independent phospholipase A2 enzyme that contains a repeated structural homologous to the integral membrane protein binding domain of ankyrin.";
RL J. Biol. Chem. 272:11118-11127(1997).
CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids. It has been implicated in normal phospholipid remodeling, nitric oxide-induced or vasopressin-induced arachidonic acid release and in leukotriene and prostaglandin production. May participate in fas mediated apoptosis and in regulating transmembrane ion flux in glucose-stimulated B-cells.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver, heart and skeletal muscle.
CC -!- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U51898; AAC53136.1; -.
DR HSSP; Q60778; IOY3.
DR RGD; 628867; Pla2g6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 6.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
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FT REPEAT 348 377 ANK 7.
FT ACT_SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBBADA7FCC99B CRC64;

Query Match 95.0%; Score 1454; DB 1; Length 751;
Best Local Similarity 94.2%; Pred. No. 4.1e-122;
Matches 274; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 LQDLMHISRRAPKPAFTLGSMDKRTDTHLLCLDGGGVKGLIIQLIIAIEKASGVATKD 60
Db 396 LQDLMPVSRARAPAFILSSMDKRTDTHLLCLDGGGVKGLVIIQLIIAIEKASGVATKD 455
QY 61 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGPYESGPLEEFKREFGE 120
Db 456 LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFGRSGPYESGPLEEFKREFGE 515
QY 121 HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRNQNNVLRPPAQPDSQVLV 180
Db 516 HTKMTDVKKPKVMTGTLSDRQPAELHLFRNYDAPEAVREPRCTPNINLKPKPTQPADQLV 575
QY 181 WRAARSSGAAPTYFRPNGRFLDGLGGLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIV 240
Db 576 WRAARSSGAAPTYFRPNGRFLDGLGGLANNPTLDAMTEIHEYNODMIRKQGNKVKKLSIV 635
QY 241 VSLGTRSPQVPVTCVDVFRPNPWLAKTVFGAKELGKMWVDDCCTDPDGR 291
Db 636 VSLGTGKSPQVPVTCVDVFRPNPWLAKTVFGAKELGKMWVDDCCTDPDGR 686

RESULT 6
Q66HD1 PRELIMINARY; PRT; 807 AA.
AC Q66HD1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feirgoid E.A., Grouse L.H., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.P., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081916; AAH81916.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RX STRAIN=C3H/He; TISSUE=Osteoblast;
RA STRAIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAH52845.1; -
DR HSSP; P07207; 1078.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AAFC CRC64;
Query Match 95.6%; Score 1463; DB 2; Length 752;
Best Local Similarity 94.8%; Pred. No. 6.4e-123;
Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 1 LODLHMSIRKPAFILSGMRDEKTHDHLCLDGGVKGGLIIQLLIAEKASGVATKD 60
DB 397 LODLMPISRKPAFILSSMRDEKSHDHLCLDGGVKGGLVLIQLLIAEKASGVATKD 456
QY 61 LFDWAGTSTGGILALAILHKSMAVMGMVFRMKDEVFGRGSRPYESGPLEFLKREFGE 120
DB 457 LFDWAGTSTGGILALAILHKSMAVMGMVFRMKDEVFGRGSRPYESGPLEFLKREFGE 516
QY 121 HTKMTDVRKPKVMTCTLSDRPAELHFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 180
DB 517 HTKMTDVRKPKVMTCTLSDRPAELHFRNYDAPETVREPRFNQNVNLRPPAQPSDQLV 576
QY 181 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNQDLIRKQANKVKLSIV 636
QY 241 VSLGTRSPQVPTVCDVFRPNPNWELAKTVFGAKELGKQVWDCCTDPDGR 291
DB 637 VSLGTRSPQVPTVCDVFRPNPNWELAKTVFGAKELGKQVWDCCTDPDGR 687
RESULT 4
Q9UK61
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ID Q9UK61 PRELIMINARY; PRT; 807 AA.
AC Q9UK61;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+-independent phospholipase A2 long form (Pla2g56 protein).
GN Name=Pla2g56;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RA Chiu C.-H., Jackowski S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259401; AAF72651.1; -
DR EMBL; BC057209; AAH57209.1; -
DR HSSP; Q60778; 10Y3.
DR MGD; MGI:1859152; Pla2g56.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;
Query Match 95.6%; Score 1463; DB 2; Length 807;
Best Local Similarity 94.8%; Pred. No. 7e-123;
Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
QY 1 LODLHMSIRKPAFILSGMRDEKTHDHLCLDGGVKGGLIIQLLIAEKASGVATKD 60
DB 452 LODLMPISRKPAFILSSMRDEKSHDHLCLDGGVKGGLVLIQLLIAEKASGVATKD 511
QY 61 LFDWAGTSTGGILALAILHKSMAVMGMVFRMKDEVFGRGSRPYESGPLEFLKREFGE 120
DB 512 LFDWAGTSTGGILALAILHKSMAVMGMVFRMKDEVFGRGSRPYESGPLEFLKREFGE 571
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RN SEQUENCE FROM N.A.
 RP MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clump M., Shink L.J., Alnsough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.P., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaubin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudon J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kuranashi H., Saitta S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dmanski J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilahun Y., Wright H.;
 RA "The DNA sequence of human chromosome 22.";
 RT Nature 402:489-495(1999).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
 RC TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udman T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodelling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

in leukotriene and prostaglandin production. May participate in
 fas mediated apoptosis and in regulating transmembrane ion flux in
 glucose-stimulated B-cells.
 -!- FUNCTION: Isoform ankyrin-iPLA2-1 and isoform ankyrin-iPLA2-2,
 which lack the catalytic domain, are probably involved in the
 negative regulation of iPLA2 activity.
 -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a carboxylate.
 -!- SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 -!- SUBCELLULAR LOCATION: Isoform LH-IPLA2 was found to be membrane
 bound. Isoform SH-IPLA2 is cytoplasmic.
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=4;
 Name=LH-IPLA2;
 IsoId=O60733-1; Sequence=Displayed;
 Name=SH-IPLA2;
 IsoId=O60733-2; Sequence=VSP_000278;
 Name=Ankyrin-iPLA2-1;
 IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
 Name=Ankyrin-iPLA2-2;
 IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 -!- TISSUE SPECIFICITY: Four different transcripts were found to be
 expressed in a distinct tissue distribution.
 -!- SIMILARITY: Contains 7 ANK repeats.

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 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 47.4624 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLHISRARKPAFLGSM.....GAKELGKVVVDCTDPTDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	99.5	806	1 PA26 HUMAN	O60733 homo sapien
2	1463	95.6	752	1 PA26 MOUSE	P97819 mus musculu
3	1463	95.6	752	2 Q7TFX2	Q7tpx2 mus musculu
4	1463	95.6	807	2 Q9JRK6	Q9jrk6 mus musculu
5	1454	95.0	751	1 PA26 RAT	P97570 rattus norv
6	1450	94.7	807	2 Q66HD1	Q66hd1 rattus norv
7	1042	68.1	756	2 Q6DDK0	Q6ddk0 xenopus lae
8	966.5	63.1	818	2 Q6NWX0	Q6nwx0 brachydanio
9	736	48.1	386	2 Q8MR13	Q8mr13 drosophila
10	736	48.1	877	2 Q9VT60	Q9vt60 drosophila
11	736	48.1	887	2 Q7KUD4	Q7kud4 drosophila
12	720	47.0	879	2 Q7Q2U1	Q7q2u1 anopheles g
13	456.5	29.8	1071	2 Q20500	Q20500 caenorhabdi
14	419	27.4	1021	2 Q810Q6	Q810q6 caenorhabdi
15	419	27.4	1023	2 Q62398	Q62398 caenorhabdi
16	376	24.6	762	2 Q95YD2	Q95yd2 caenorhabdi
17	287	18.7	501	2 Q9N5L3	Q9n5l3 caenorhabdi
18	270.5	17.7	525	2 Q9TVS0	Q9tvs0 caenorhabdi
19	266	17.4	546	2 Q8MXR3	Q8mxr3 caenorhabdi
20	260	17.0	433	2 Q7Q158	Q7q158 anopheles g
21	255	16.7	1285	2 Q80693	Q80693 arabidopsis
22	253.5	16.6	456	2 Q22152	Q22152 caenorhabdi
23	235.5	15.4	355	2 Q9KVG8	Q9kvg8 vibrio chol
24	230.5	15.1	552	2 Q6JBI3	Q6jbi3 dictyocaulu
25	230	15.0	459	2 Q6JBI2	Q6jbi2 dictyocaulu
26	222	14.5	361	2 Q6XGD7	Q6xgd7 escherichia
27	213.5	13.9	679	2 Q96L76	Q96l76 plasmodium
28	211.5	13.8	380	2 Q95035	Q95035 homo sapien
29	211.5	13.8	639	2 Q9H7T5	Q9h7t5 homo sapien
30	211.5	13.8	782	2 Q9NPF80	Q9npf80 homo sapien
31	210.5	13.7	776	2 Q8K1N1	Q8k1n1 mus musculu

32 210.5 13.7 803 2 Q9DC20
33 204.5 13.4 577 2 Q9K5M3
34 201 13.1 382 2 Q9M1W9
35 201 13.1 384 2 Q93ZQ3
36 199.5 13.0 671 2 Q7RK61
37 198 12.9 390 2 Q8YUN7
38 193.5 12.6 387 2 Q671Z1
39 191 12.5 332 2 Q62AP1
40 191 12.5 332 2 Q63JR4
41 190.5 12.4 1294 2 Q7SF66
42 188 12.3 322 2 Q7POX4
43 188 12.3 1409 2 Q69VY8
44 187 12.2 302 2 Q73HJ4
45 185.5 12.1 401 2 Q9FIY1

ALIGNMENTS

RESULT 1
PA26_HUMAN STANDARD; PRT; 806 AA.
AC O60733; Q75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (iPLA2) (Cal-
PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonym=IPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND
RP ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent
RT phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancreatic islets;
RX MEDLINE=99194813; PubMed=10092647; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct
RT catalytically active isoforms of group VI phospholipase A2 (iPLA2)
RT that arise from an exon-skipping mechanism of alternative splicing of
RT the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616(1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes
RT with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RX Ansoorge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND
RP THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;
RT "NIHNS-SNPs, environmental genome project, NIHNS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

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Db      17  ILSDGGVGRGIIAGVILAFLEKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 76
QY      84  MAYMRGMYFRMKDEYFRGSRPYE-----SGP-----LEE 112
Db      77  TG---RPHPAAKDIV-----PFYLEHCPKIFPQPTGVALLPKLLSGPKYSGKYLRLN 128
QY     113  FLKREFGE---HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNL 169
Db     129  LLSKLLGETRLHQTLTNI-----VIPTFDIKLQPT---IFSSY---QLLVDPSLDVKV-- 176
QY     170  RPPAQPSDQVWRAARSSGAAPTYFRPN-----GRFLDGGLLANNPTLDAMT 216
Db     177  -----SDICI-----GTSAAITFPFPHYFNSQGNKTEFNLDGAVTANNPTLVAMT 225
QY     217  -----EIHEYNDLIRKQANKVKLS-----IVVSLGTG 246
Db     226  AVSKQIVKNNPDM-----GKLKPLGDFRFLVISIGTG 257
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RESULT 15

H85437

patatin-like protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: H85437

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: H85437

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <STO>

A:Cross-references: UNIPROT:O23179; GB:NC_001268; NID:g7270656; PIDN:CAB80373.1; GSPDB:G

C:Genetics:

A:Gene: AT4g37070

A:Map position: 4

C:Superfamily: patatin

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Query Match      11.5%; Score 176; DB 2; Length 414;
Best Local Similarity 26.6%; Pred. No. 5.5e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY     30  LCLDGGGVKGIIIIQLLIAIEK-----ASGVATKDLFDWVAGTGTGILAILHSHKS 83
Db     21  ILSDGGVGRGIIAGVILAFLEKQLQELDGEARLADYFDVIAGTGTGGLVTAMLTVPDE 80
QY     84  MAYMRGMYFRMKDEYFRGSRPYE-----SGP-----LEE 112
Db     81  TG---RPHPAAKDIV-----PFYLEHCPKIFPQPTGVALLPKLLSGPKYSGKYLRLN 132
QY     113  FLKREFGE---HTKMTDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNL 169
Db     133  LLSKLLGETRLHQTLTNI-----VIPTFDIKLQPT---IFSSY---QLLVDPSLDVKV-- 180
QY     170  RPPAQPSDQVWRAARSSGAAPTYFRPN-----GRFLDGGLLANNPTLDAMT 216
Db     181  -----SDICI-----GTSAAITFPFPHYFNSQGNKTEFNLDGAVTANNPTLVAMT 229
QY     217  -----EIHEYNDLIRKQANKVKLS-----IVVSLGTG 246
Db     230  AVSKQIVKNNPDM-----GKLKPLGDFRFLVISIGTG 261
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Search completed: May 26, 2005, 14:20:33
Job time : 10.359 secs

A:Cross-references: UNIPROT:Q9YUN7; GB:BA000019; PIDN:BA074001.1; PID:g17131394; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2302
C:Superfamily: patatin

Query Match 12.9%; Score 198; DB 2; Length 390;
Best Local Similarity 24.3%; Pred. No. 5.1e-10;
Matches 68; Conservative 40; Mismatches 78; Indels 94; Gaps 10;

QY 30 LLCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTSTGGILALAILHKSMA 85
Db 5 ILSLDGGGIRGVITARILEOVRQIOQQQKSLHEYFDLTAGTSTGIIITAGIAAKNS 64
QY 86 YNRGMVFRMKDEVFRGSRP--YESGP-----LEEF-----LKRFGHEHTKM 124
Db 65 ELVOLYQEOGKQIFPTERKERYKIPSFLOPLIEAFSLPKYSHOGLINVLKVLGD-TRK 123
QY 125 TVVRKPKVMLTG-----TISDRQPAELHLFRNYDAPETVREPRFNQNVN 168
Db 124 KDVESPIMLILAVDTLYRNTFTFNCHPDLDGRWYDDCHL----- 163
QY 169 LRPPAQPSQOLVWRAARSSGAPTYFRP-----NGRF--LDGGLANNPTLDA 214
Db 164 -----WEICTASTAAPTFFPPYKLEFPVKNKEKYNWVFPFHIDGGVAANNPALAA 211
QY 215 MTEIHEYNODLIRKGOANKVKLSI-----VVSIGTGHS 248
Db 212 LSLWRLSOSSVSAIKQKYNLDGINLEDAIILSIGTGT 251

RESULT 12
G85437
patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <STO>
A:Cross-references: UNIPROT:O23180; GB:NC_001268; NID:g7270655; PIDN:CAB80372.1; GSPDB:G
A:Gene: AT4g37060
A:Map position: 4
C:Superfamily: patatin

Query Match 11.9%; Score 182; DB 2; Length 414;
Best Local Similarity 27.3%; Pred. No. 1.6e-08;
Matches 73; Conservative 34; Mismatches 84; Indels 76; Gaps 13;

QY 30 LLCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTSTGGILALAILHKS 83
Db 21 ILSLDGGGVRGIAGVILAYLEKQLQELDGEHVRVADYFDVIAGTSTGGLVMTAPDE 80
QY 84 MAYMR-----GMVFRMKDEVFRGSRPYESGPLE-----BFLKREFGE 120
Db 81 NGRPRFAAKEIYVFFYLEHCPKIF---PQPTGVALLPKLXLLSGPKSGNYLRTLGK 136
QY 121 ----HYKMTDVRKPKVMTLTISDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQPSD 177
Db 137 LLGETKLRQTLTNVVIPTFDIKTLQPT---IFSSYQA---LTDPSLDVRV-----SD 182
QY 178 QLVWRAARSSGAPTYFRP-----NGRFLDGLANNPTLDAMT-----EIHE 220
Db 183 ICI-----GTSAAPTYFPFYSNEDSQKTRHFNLDVGGVTANNPTLVAMTAVTKQIVN 237
QY 221 YNQDLIRKGOANKV-KKLSIVVSLGTG 246

A:Cross-references: UNIPROT:O23180; GB:NC_001268; NID:g7270655; PIDN:CAB80372.1; GSPDB:G
A:Gene: AT4g37060
A:Map position: 4
C:Superfamily: patatin

Db 238 NNPDN---GTLNPLGYDQFLVISIGTG 261

RESULT 13
F85437
patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:O23181; GB:NC_001268; NID:g7270654; PIDN:CAB80371.1; GSPDB:G
C:Genetics:
A:Gene: AT4g37050
A:Map position: 4
C:Superfamily: patatin

Query Match 11.7%; Score 179; DB 2; Length 428;
Best Local Similarity 26.5%; Pred. No. 3.1e-08;
Matches 72; Conservative 41; Mismatches 81; Indels 78; Gaps 14;

QY 30 LLCLDGGGVKGLIIQLLIAIEKASGVATK--DLFDWVAGTSTGG-ILALAILHKS 82
Db 37 ILSIDGGGIRGIIPGTILAYLESQQLQELDGEARLVDFVISGTSTGGLIVAMLTADQ 96
QY 83 SMAYMRG-----MYFRMKDEVFRGSR-----PYESGPLEEF 113
Db 97 SGCHSNNRPLFEAKEIVPFLKSPKIFPPQPRGIFCGWGTIVLVGGPKFNGKYLHD 156
QY 114 LKREFGEHTMTDVRKPKVMTLTISDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPA 173
Db 157 LVGEGLDITKLTQSLTNVVIPCFDIKKLQPV---IFSSYQAVN-----NQAMN---A 202
QY 174 QPSDQLVWRAARSSGAPTYFRPNGRF-----LDGGLANNPTLDAMTEIH 219
Db 203 KLSIDICI-----STSAAPTFF-PAHRFTNEDSEKIHFNLDGGIAANNPTLCAIAEV- 255
QY 220 EYNQDLIRKGOA-NKVKKLS-----IVVSLGTG 246
Db 256 --TKQIIKKNFVNGDISPLDFTFRFLVISIGTG 285

RESULT 14
T52294
patatin-like protein [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52294
R:Terry, N.; Heijnen, L.; De Keyser, A.; Van Asseltonck, M.; De Clercq, R.; Verbakel, H.
ueller, C.; Mayer, K.; Dehais, P.; Rombauts, S.; Van Montagu, M.; Rouze, P.; Vos, P.
PBES Lett. 445, 237-245, 1999
A:Title: Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by seq
A:Reference number: Z26022; MUID:99192287; PMID:10094464
A:Accession: T52294
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-410 <TER>
A:Cross-references: UNIPROT:O23148; EMBL:AJ002596; PIDN:CAA05628.1
C:Genetics:
A:Map position: 4
C:Superfamily: patatin

Query Match 11.5%; Score 176; DB 2; Length 410;
Best Local Similarity 26.6%; Pred. No. 5.4e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY 30 LLCLDGGGVKGLIIQLLIAIEK-----ASGVATKDLFDWVAGTSTGGILALAILHKS 83

R.Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertes, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: AV1600; MUID:99021743; PMID:9804551
A:Accession: G71615
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-679 <GAR>
A:Cross-references: UNIPROT:O96176; GB:AE001393; GB:AE001362; NID:g3845175; PIDN:AAC7187
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0410C

Query Match 13.9%; Score 213.5; DB 2; Length 679;
Best Local Similarity 27.7%; Pred. No. 4.3e-11;
Matches 71; Conservative 37; Mismatches 95; Indels 53; Gaps 8;
QY 30 LILCLDGGVKGILIIQLLIAIEKASGVATK-----DLFDWVAGTSTGGILALAIL 79
DB 337 ILSLDGGGI---LTISTLLVLRLEAELEKEIGSDDIKLIDCFDMVCGTSGAGLSLALL 393
QY 80 HSKSMAYRGMVFRMKDEVRGSRPVESGPLEE-----ELKREGEHTKMTDVRK 129
DB 394 REIDLDQVSNMWPSTIKKVFEGNRMIISGIFEGDVNNKDVFLERMGNKF--WSSYKK 451
QY 130 PKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDOLVWRAARSSGA 189
DB 452 FYCFVTATDVKHKPKYKFLIRNYTHKYSINAEVDGINKVP-----LWLAAWATAS 503
QY 190 ARTY-----FRNGRFLDGLLANNPTLDAMTEIHEYNOQLIRKQANKV 234
DB 504 APTYLKGPSAEDIKKLGINIKPEIHLVDGALKASNPALTBECARLN---NKNLSIFI 559
QY 235 KK-LSIIVWSLGTGRSP 249
DB 560 KEDLDLTVLSIGTGQVP 575

RESULT 9
JC7284
phospholipase A2 (EC 3.1.1.4) 2, calcium-independent - human
N:Alternate names: membrane-associated calcium-independent phospholipase A2
C:Species: Homo sapiens (man)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JC7284
R:Tanaka, H.; Takeya, R.; Sumimoto, H.
Biochem. Biophys. Res. Commun. 272, 320-326, 2000
A:Title: A novel intracellular membrane-bound calcium-independent phospholipase A2.
A:Reference number: JC7284
A:Accession: JC7284
A:Molecule type: mRNA
A:Residues: 1-782 <TAN>
A:Cross-references: UNIPROT:Q9NP80; DDBJ:AB041261
C:Genetics:
A:Gene: ipla2-2
A:Map position: 7q31
C:Keywords: carboxylic ester hydrolase; membrane-associated protein

Query Match 13.8%; Score 211.5; DB 2; Length 782;
Best Local Similarity 28.5%; Pred. No. 8e-11;
Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;
QY 16 ILGSRMRDEKRTDHLCLDGGVKGILIIQLLIAIEKASGVATKDLFDWVAGTSTGGILAI 75
DB 430 LIGYDVPVKGRIILSIDGGTGRGVVALQTLKLVLTQKPVHQLFDYICGVSTGAILA 489
QY 76 LAI-LHKSMAVMYRMGMKDEVR-----GSRPYESGPLEEFLKRFEGEHT 122
DB 490 FMLGLFHMPLDECEELYRKLKSGDVFQSNVIVGVTKMSWSHAFYDSQTNWENILKDRMGSA 549
QY 123 KMTDVRK---PKVMLTGTLSDRQ-PAELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQ 178

Db 550 MIETARNPTCPKVAAVSTIVNRGITPKAFVFRNYG-----HPPGINSHY-----LGGCOY 599
QY 179 LVWRAARSSGAAPTYFRP-----NGRFLDGLLANNPTLDAMTEIHEYNOQLIRKQANKV 234
DB 600 KMWQAIRASSAAGPYFAEYALGNDLHQDGLLLNPNPSALAMHECKCLPVDV-----650
QY 235 KKLISIVWSLGTGR 247
DB 651 -PLECIVSLGTGR 662

RESULT 10
T48109
hypothetical protein F16M2.50 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48109
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T48109
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <RIB>
A:Cross-references: UNIPROT:Q9MIW9; EMBL:AL138648
A:Experimental source: cultivar Columbia; BAC clone F16M2
C:Genetics:
A:Map position: 3
A:Introns: 313/3
A:Note: F16M2.50
C:Superfamily: patatin

Query Match 13.1%; Score 201; DB 2; Length 382;
Best Local Similarity 26.7%; Pred. No. 2.7e-10;
Matches 75; Conservative 38; Mismatches 94; Indels 74; Gaps 12;

QY 4 LMHISRARKPAFILGSRMEDEKRTDHLCLDGGVKGILIIQLLIAIEKASGVAT-----58
DB 19 LSHCDSRK-----TRILSIDGGTGTGIVAAASILHLEHQILQTDGPHA 63
QY 59 --KDLFDWVAGTSTGGILALILHS-----KSMAYMRGMVFRMK-DEVFRG 101
DB 64 HISDFDIVAGTGTGGILALILVADGSGRPMFTARDAVKFAEKNSELSFEIRYTCVFR 123
QY 102 SRPYESGPLEBFL-----KREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPET 157
DB 124 NKRYSGKSMERVLETAFRREDGKVLTKMDTKCPKLVPCVDLKTAP---FVFSRAGASES 180
QY 158 VREPRFNQNVNLRPPAOPSDOLVWRAARSSGAAPTYFRP-----NGR-----FLDGLLLA 207
DB 181 ---PSF-----DFELWKVCRATSATPSLFPFVSVDGKTSCSAVDGGLVM 224
QY 208 NNPTLDAMTEIHEYNOQLIRKQANKVKKLISIVWSLGTGRS 248
DB 225 NNPTAAATHVLNKRDP---PSVNGVDDL-LVLSLNGGPS 261

RESULT 11
AG2093
patatin-like protein (imported) - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AG2093
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.;
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2093
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <KUR>

A;Reference number: Z14574
A;Accession: T02131
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1265 <V>
A;Cross-references: UNIPROT:O80693; EMBL:AC004392; NID:g3282170; PID:g3367519; GSPDB:GN000022; CESP:T04B2.5
C;Genetics:
A;Gene: ATSP:F8K4.6
A;Map position: 1
A;Introns: 146/3; 196/1; 229/1; 297/3; 379/3; 434/1; 521/1; 561/3; 615/3; 683/1; 728/3;
C;Superfamily: Arabidopsis thaliana hypothetical protein F8K4.6

Query Match 16.7%; Score 255; DB 2; Length 1265;
Best Local Similarity 28.7%; Pred. No. 1.8e-14;
Matches 81; Conservative 39; Mismatches 90; Indels 72; Gaps 8;

QY 30 LLCLDGGGVKGLIIIOILLIAIEKASGATVATKDLFDWAGTSTGGILALAI-LHKSXWAYMR 88
Db :
455 ILTMDDGGMKGLATVQLIKEIGSKPIHELFDLCGTSTGGMLAIALGVKLMTLEQQE 514
QY 89 GMTFRMKDEVFGRSRP-----YESGP-----LEEF 113
Db :
515 EIYNKLGKLVFAESVPKDNEAAAWREKLDLYKSSQSFRVWIHGSHKSANEFERLLKEM 574
QY 114 LKRFEGHETKMTDVVK-PKVMLTGTLSDROPALHLIFRNYDAPETVREPRF----NONVN 168
Db :
575 CADEDGDLLATESAVKNVPKFVVVTVLSVMPAQPFIFRNYYQYPVGTPENSYAFSDHSOGS 634
QY 169 LRPPAPSDDL-----VWAARSQAAPTFF-----RPNGRLDGGLLA 207
Db :
635 TLTSSTASDAQGYKYOSAFWGCKHQVQWQAIRASSAAPYYLLDDPSVGTNYSRWODGAIVA 694
QY 208 NNPTLOAMTEIHEYNODLIIRKGQANKVKKLSIVVSLGTGRSP 249
Db :
695 NNFTIFAIRAQLLPD-----TKIDLVSIGSGSV 726

RESULT 6
T24442
hypothetical protein T04B2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24442; T26042
R;Coles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19890
A;Accession: T24442
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-456 <WL>
A;Cross-references: UNIPROT:Q22152; EMBL:Z68299; PIDN:CAA92615.1; GSPDB:GN000022; CESP:T04B2.5
A;Experimental source: clone T04B2
R;Coles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z20141
A;Accession: T26042
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-456 <WT2>
A;Cross-references: EMBL:Z68301; PIDN:CAA92628.1; GSPDB:GN000022; CESP:T04B2.5
A;Experimental source: clone W01B6
C;Genetics:
A;Gene: CESP:T04B2.5
A;Map position: 4
A;Introns: 48/3; 104/3; 139/1; 424/3
C;Superfamily: patatin

Query Match 16.6%; Score 253.5; DB 2; Length 456;
Best Local Similarity 32.3%; Pred. No. 5.9e-15;
Matches 86; Conservative 41; Mismatches 76; Indels 63; Gaps 14;

QY 5 MHTSRARKPAFIIGSMRDEKTRTHLLCLDGGGVKGLI-IIQLLIAEKASGVAT-KDLF 62
: :

Db 112 IQINRSKKVDGVMA-----LCLDGGGRMLGVSVVCLLYASRRLLGDETLPNLF 159

QY 63 DWVAGTSTGGILALAILHKSMAVMRGMYFRMKDEVF-RGSRPYESGPLEEFLKREFGEH 121

Db 160 DWFIGTSGMLALSMVKNKISISCFQYWDMSQIFLRGST-----VKRLLGQ 209

QY 122 TKMTDVRKPKVM-----LTGTLSD-----RQPAELHLFRNYDAPETVREPRN 164

Db 210 VAVQTKNIDKVLGDCPFTQTLQECPTRLTIPALDITAPARLHVFRNYSFTKPPGAP-LN 268

QY 165 QNVNLRPPAOPSQDLVWRAARSSGAAPTYFRP-----NGRFLDGLLANNPTLDAMTEIHE 220

Db 269 ED-----QDVLFRNARASGAAPTYFEPFYGNKVLVDGSAFVANYP-LNVL--FKE 316

QY 221 YNODLIRKQANKVKKLSIVVSLGTG 246

Db 317 Y--DSFSKHQ--QPIHLGVLISGTG 338

RESULT 7

patatin-related protein VC0178 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: E82354

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: E82354

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-355 <HEI>

A:Cross-references: UNIPROT:Q9KVG8; GB:AE004108; GB:AE003852; NID:g9654578; PIDN:AAF93354

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0178

A:Map position: 1

C:Superfamily: patatin

Query Match 15.4%; Score 235.5; DB 2; Length 355;

Best Local Similarity 29.2%; Pred. No. 1.8e-13;

Matches 75; Conservative 38; Mismatches 83; Indels 61; Gaps 9;

QY 27 HDHL-----LCLDGGGVKGLIIQLLIAIK-----ASGVATKDLFDWVAGTSGII 73

Db 7 YEHLQNVRLSLNGGARGLFTISLAEIERIIEEKOGINGFKVDYFDLITGTSIGGI 66

QY 74 LALAILHKSMAVMRGMY-----FRMKDEVPRGSRPYESGPLEEFL 114

Db 67 LALGLAYGKSARELEDVFRKQAGYIFPEQKYPFRFPVRRYRLARGPL-YDSKPLAKTY 125

QY 115 KRFBGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAQ 174

Db 126 ASMWGEESTNDLRCRVLIPTVNLSTGPK---QFFKTPHNPEFHRDGRIK----- 172

QY 175 PSQDLVWRAARSSGAAPTYFRP-----NGRFLDGLLANNPTLDAMTEIHEYNQDLIRK 228

Db 173 -----LTDALATSAPTYFAPHYCVDLDSYFADGGLVANNP---SFGLHEVFRDMATD 224

QY 229 GQANKVKKLSIVVSLGT 245

Db 225 FPEAKVSDVKI-LNVGT 240

RESULT 8

G71615

phospholipase A2-like a/b fold hydrolase PF0410c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C:Accession: G71615

A:Accession: T22327
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1071 <W1>
A:Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F4
A:Experimental source: Clone F47A4
C:Genetics:
A:Gene: CESP:F47A4.5
A:Map position: X
A:Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 29.8%; Score 456.5; DB 2; Length 1071;
Best Local Similarity 34.5%; Pred. No. 7.4e-33;
Matches 102; Conservative 62; Mismatches 97; Indels 35; Gaps 8;

QY 1 LQDLMHISARKPAFILGSMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 730 IQDTLGGSRGKKAKV-----NLISMDGGGIRGLVITQLIAIEERLGDIFK 777

QY 61 LFDWAGTSTGILALAILHSKSMAYMRGMVFRMKDEVPFRG--SRPYESGPLEEFKRBPG 119
DB 778 YFDWAGTSTGILAGLTKSLREMQOYLLKDRVDFGIMPPYDTVQLEKFIQDQFG 837

QY 120 EHTKMDVRKPKVMTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOPDOL 179
DB 838 TGT-VWEIPYKIMISAVNSEKLPVRLEWARYKPAKV-----APETPKEMP 884

QY 180 VVRAARSGAAPTFRPN--GRFLDGLLANNPTLDAMTEIHEYNOQLIRKQKVKKLS 238
DB 885 LWMALRRSTAAFPVLPKPSDRIDGGIISNNPALDLMSVHAYNRELQSLGRKSDAVQMN 944

QY 239 IVVSLGTGRSPQPVTCVDVFR--PSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
DB 945 VLVSFQGTG---QTPSTVIETLSIDNSPLQSIKTI----KNLAAMFTDOATSEGAP 994

RESULT 3
T26261
hypothetical protein W07A8.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26261; T26892
R:Basham, V.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20184
A:Accession: T26261
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1023 <W1>
A:Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CAB04932.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone W07A8
R:Ainscough, R.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20281
A:Accession: T26892
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1023 <W12>
A:Cross-references: EMBL:AL021489; PIDN:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2
A:Experimental source: clone Y44A6C
C:Genetics:
A:Gene: CESP:W07A8.2
A:Map position: 5
A:Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 70

Query Match 27.4%; Score 419; DB 2; Length 1023;
Best Local Similarity 33.9%; Pred. No. 1.8e-29;
Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;

QY 17 LGSMDREKTHD--HLLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGTL 74
DB 678 LKELVEKKTISNVINVLGDDGGIRGLVTVQMLICLAEFLDRPLIDYFDWIGATSTGCYI 777

QY 75 ALAILHSKSMAYMRGMVFRMKDEVPFRG--SRPYESGPLEEFKRBPGHETKMTDVRKPKVM 133
DB 738 MSTMTGSLRKAQRYYLMPFDQDLFSWTRFYDTTKLETFIQARFAGADRLMGDIKYPRFF 797

QY 134 LTGTLSDRQPAELHLFRNYDAPETVREPRFNQNVNLRPPAOPDOLVVRAARSSGAAPT 193
DB 798 CTTVRADTFPQLELLRNYRLPISEKE---NNDLGF---TDNELTIWKATERSAAPTY 851

QY 194 FRPN--GRFLDGLLANNPTLDAMTEIHEYNOQLIRKQKVKKLSIVVSLGTGRSPQVP 252
DB 852 FSASEGKFDGMSISNNPVLDMSDIGFYNTTCQGRIPERKMDMGCVLSVGTGITPICP 911

QY 253 VTCVDVFRPSNPWELAKTVFGAKELGKMWVDCCTDPDGRP 292
DB 912 VD-PSVFMNDLFGMLR---GMKNLSLVVIDOATGAP 947

RESULT 4
T33857
hypothetical protein D1037.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33857
R:Ledwith, J.; Biewald, T.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of C. elegans cosmid D1037.
A:Reference number: Z21424
A:Accession: T33857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-468 <LED>
A:Cross-references: EMBL:AF106592; PIDN:AAC78490.1; GSPDB:GN00019; CESP:D1037.5
A:Experimental source: strain Bristol N2; clone D1037
C:Genetics:
A:Gene: CESP:D1037.5
A:Map position: 1
A:Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 17.0%; Score 261; DB 2; Length 468;
Best Local Similarity 29.8%; Pred. No. 1.3e-15;
Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

QY 16 ILGSMRDEKTHD--LLCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWAGTSTGGTL 74
DB 180 VLASEKKQWPEERVLLALDGGIRAVITIQMLIHIDYLLGGLVEKLLDIAGTSCGGVI 239

QY 75 ALAI--LHSKSMAYMRGMVFRMKDEVF--RGSR---PYESGPLEEFKREF--GEHTKMTDV 127
DB 240 TLLSTNNRNIETRKILLDMRDRVIRGADKAVPKYSNGMEYIARHVTTWEDSKMSI 299

QY 128 RPKVYMLTGTLSDRQPAELHLFRNY--DAPETVREP--RFNQNVNLRPPAOPDQLVWRAA 184
DB 300 KHRRAIVTVADTRMVPVQLLLFRSYRPEMPEACSHYKF-----LDPTKVELWKT 350

QY 185 RSSGAAPYFRPNGRFLDGLLANNPTLDAMTEIHEYNOQLIRKQKVKK-----K 236
DB 351 RCTTAAPYFFESFNGSLSDGGLIANNPTLALISDFLTNK--LEKSFASKSSSERENRGNWK 408

QY 237 LSVVSLGTGRSPQVPVTCVDV 258
DB 409 IGCVISLGTGVFPTEKIDGL 430

RESULT 5
T02131
hypothetical protein F8K4.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02131
R:Vystotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, S.; Li, ritz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.
submitted to the EMBL Data Library, August 1998
A:Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 8.35905 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LQDLMHISRARKPAFILGSM.....GAKELGKMVVDCTDPDGRP 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	99.5	851	2 T12503	hypothetical prote
2	456.5	29.8	1071	2 T22327	hypothetical prote
3	419	27.4	1023	2 T26261	hypothetical prote
4	261	17.0	468	2 T33857	hypothetical prote
5	255	16.7	1265	2 T02131	hypothetical prote
6	253.5	16.6	456	2 T24442	hypothetical prote
7	235.5	15.4	355	2 E82354	patatin-related pr
8	213.5	13.9	679	2 G71615	phospholipase A2-1
9	211.5	13.8	782	2 JC7284	phospholipase A2 (
10	201	13.1	382	2 T48109	hypothetical prote
11	198	12.9	390	2 AG2093	patatin-like prote
12	182	11.9	414	2 G85437	patatin-like prote
13	179	11.7	428	2 P85437	patatin-like prote
14	176	11.5	410	2 T52394	patatin-like prote
15	176	11.5	414	2 H85437	patatin-like prote
16	174.5	11.4	390	2 T03841	patatin homolog -
17	164	10.7	499	2 T02580	hypothetical prote
18	163	10.6	405	2 T10260	patatin-like prote
19	161	10.5	407	2 T00989	hypothetical prote
20	158.5	10.4	388	2 T10770	patatin-like latex
21	158.5	10.4	490	2 B97815	patatin b1 precurs
22	151.5	9.9	388	2 T10765	patatin-like latex
23	151.5	9.9	388	2 T10763	patatin-like latex
24	150.5	9.8	494	2 D71665	patatin b1 precurs
25	147	9.6	526	2 T08541	hypothetical prote
26	146	9.5	386	2 T07592	class I patatin -
27	140	9.1	386	2 A29810	patatin - potato
28	139	9.1	386	2 A26017	patatin T5 precurs
29	138	9.0	377	2 S05593	patatin precursor

30	138	9.0	386	2 S51596	patatin precursor,
31	137	8.9	320	2 F70034	conserved hypothet
32	137	8.9	384	2 A24142	patatin precursor
33	134	8.8	386	2 S05592	patatin precursor
34	134	8.8	386	2 B26017	patatin T58 precur
35	129.5	8.5	488	2 T06725	hypothetical prote
36	124	8.1	318	2 D24923	TEG protein - Bac
37	116	7.6	324	2 D70943	hypothetical prote
38	112	7.3	473	2 T28118	hypothetical prote
39	108	7.1	329	2 A87087	conserved hypothet
40	103	6.7	610	2 B87518	conserved hypothet
41	96.5	6.3	296	2 E84000	hypothetical prote
42	95	6.2	598	2 E71657	hypothetical prote
43	94	6.1	314	2 AF3365	serine proteinase
44	91	5.9	260	2 H69874	conserved hypothet
45	90.5	5.9	254	2 G72343	conserved hypothet

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFP434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12503
R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17527
A:Accession: T12503
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <ANS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFP434A102
C:Genetics:
A>Note: DKFP434A102.1

Query Match 99.5%; Score 1524; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 7.8e-130;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LQDLMHISRARKPAFILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD	60
DB	496	LQDLMHISRARKPAFILGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD	555
QY	61	LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE	120
DB	556	LFDWVAGTSTGGILALAILHLSKSMAYMRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGE	615
QY	121	HTKMTDVRPKVMTGTLSDRQPAELHLFRNYDAPETVREPRENQVNLRPPAQPSDQIV	180
DB	616	HTKMTDVRPKVMTGTLSDRQPAELHLFRNYDAPETVREPRENQVNLRPPAQPSDQIV	675
QY	181	WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANVKKLSIV	240
DB	676	WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANVKKLSIV	735
QY	241	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPDGR	291
DB	736	VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDCTDPDGR	786

RESULT 2

T22327
hypothetical protein F47A4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22327
R:Northmore, B.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19549

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-2

Query Match 88.1%; Score 1837; DB 2; Length 752;
Best Local Similarity 87.3%; Pred. No. 4.4e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
QY 1 MOFFGRLVNTFSGVNTLFSNPFVRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTLSSVNTLFSNPFVRKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
DB 61 SPRNPHSGFRLQLESEADALVNFQFSSQLPPFYESSVQVLHVEVLQHLSDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEIILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRGDSEIILVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCINMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCINMGPSGFPPIHTAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNVTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGTPLHLAMSK 360
DB 301 RMLLKRGCDVDSTSAAGNTALHVAVMNRFDCAIVLLTYGANAGTPEHGTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKI 393
DB 361 DNMEMIKALIVFGAEVDTNDPFGTPTAFWASKI 393

RESULT 15

US-09-519-223-2
Sequence 2, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-2

Query Match 88.1%; Score 1837; DB 3; Length 752;
Best Local Similarity 87.3%; Pred. No. 4.4e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
QY 1 MOFFGRLVNTFSGVNTLFSNPFVRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTLSSVNTLFSNPFVRKEISVADYTSHERVREEGQLILFQNASRTWDCILV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVLOHLDLIRNHPSW 120
DB 61 SPRNPHSGFRLQLESEADALVNFQFSSQLPPFYESSVQVLHVEVLQHLSDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEIILVELVOYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRGDSEIILVELVOYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAHYAVQGDNSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCINMGPNGYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCINMGPSGFPPIHTAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNVTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHGTPLHLAMSK 360
DB 301 RMLLKRGCDVDSTSAAGNTALHVAVMNRFDCAIVLLTYGANAGTPEHGTPLHLAISK 360
QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKI 393
DB 361 DNMEMIKALIVFGAEVDTNDPFGTPTAFWASKI 393

Search completed: May 26, 2005, 14:21:56
Job time : 20.5289 secs

QY 361 DNMEMIKALIVFGAEVDTNDGFTPTFLASKI 393
||:|||||
Db 361 DNMEMIKALIVFGAEVDTNDGFTPTAFWASKI 393
||:|||||

RESULT 12

US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match 88.1%; Score 1837; DB 1; Length 752;

Best Local Similarity 87.3%; Pred. No. 4.4e-195;

Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVTLNLSNPRVRKEVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
|||||
Db 1 MOFGRLVNTLSSVTNLSNPRVRKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
|||||
QY 61 NPNRSQSGFRLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVLOHLTLIRNHPSW 120
|||||
Db 61 SPRNPHSGFRLFOLESEADALVNFQFSSQLPFYESSVQVLHVEVLQHLSDLIIRSHPSW 120
|||||
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDSGLVELVQYCHTQMD 180
|||||
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSGLVELVQYCHQMD 180
|||||
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
|||||
Db 181 VTDNKGETAFAHYAVQGDNSQVLLGKGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
|||||
QY 241 LCNARCNTMGPNGYPIHSAKMSQKGCARMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
|||||
Db 241 LCNARCNTMGPSGFPPIHTAMKFSQKGCARMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
|||||
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
|||||
Db 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRNFDCAIVLLTHGANADARGEHNTPLHLAISK 360
|||||
QY 361 DNMEMIKALIVFGAEVDTNDGFTPTFLASKI 393
||:|||||
Db 361 DNMEMIKALIVFGAEVDTNDGFTPTAFWASKI 393
||:|||||

RESULT 13

US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 88.1%; Score 1837; DB 2; Length 752;

Best Local Similarity 87.3%; Pred. No. 4.4e-195;

Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVTLNLSNPRVRKEVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
|||||
Db 1 MOFGRLVNTLSSVTNLSNPRVRKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
|||||
QY 61 NPNRSQSGFRLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVLOHLTLIRNHPSW 120
|||||
Db 61 SPRNPHSGFRLFOLESEADALVNFQFSSQLPFYESSVQVLHVEVLQHLSDLIIRSHPSW 120
|||||
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDSGLVELVQYCHTQMD 180
|||||
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSGLVELVQYCHQMD 180
|||||
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
|||||
Db 181 VTDNKGETAFAHYAVQGDNSQVLLGKGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
|||||
QY 241 LCNARCNTMGPNGYPIHSAKMSQKGCARMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
|||||
Db 241 LCNARCNTMGPSGFPPIHTAMKFSQKGCARMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
|||||
QY 301 RMLLRKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
|||||
Db 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRNFDCAIVLLTHGANADARGEHNTPLHLAISK 360
|||||
QY 361 DNMEMIKALIVFGAEVDTNDGFTPTFLASKI 393
||:|||||
Db 361 DNMEMIKALIVFGAEVDTNDGFTPTAFWASKI 393
||:|||||

RESULT 14

US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

US-09-927-180-23

Query Match 100.0%; Score 2084; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKFESQKGCAMIISMDSSQIHSKDPYRGASPLHWAENA 300
DB 241 LCNARCNIMGPNGYPIHSAKFESQKGCAMIISMDSSQIHSKDPYRGASPLHWAENA 300

QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360

QY 361 DNVEKIKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 361 DNVEKIKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 10

US-09-949-016-10948
; Sequence 10948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10948
; LENGTH: 819
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10948

Query Match 99.7%; Score 2078; DB 4; Length 819;
Best Local Similarity 99.7%; Pred. No. 7.5e-222;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 14 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 73

QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPSW 120
DB 74 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPSW 133

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180

DB 134 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 193

QY 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

DB 194 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 253

QY 241 LCNARCNIMGPNGYPIHSAKFESQKGCAMIISMDSSQIHSKDPYRGASPLHWAENA 300

DB 254 LCNARCNIMGPNGYPIHSAKFESQKGCAMIISMDSSQIHSKDPYRGASPLHWAENA 313

QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360

DB 314 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 373

QY 361 DNVEKIKALIVFGAEVDTNDFGETPTFLASKIG 394

DB 374 DNVEKIKALIVFGAEVDTNDFGETPTFLASKIG 407

RESULT 11

US-08-281-193-2
; Sequence 2, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-281-193-2

Query Match 88.1%; Score 1837; DB 1; Length 752;
Best Local Similarity 87.3%; Pred. No. 4.4e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60

QY 61 NPNRSQSGFRLFQLEADALVNFHQSOLLPPFYESSQVLTHTVQLHLDLIRNHPSW 120
DB 61 SPRNPHSGFRLFQLEADALVNFQFSQSPFPFYESSQVLTHTVQLHLDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEBGCTPLHLACRKGDSIILVELVQYCHQMD 180

QY 181 VTDYKGETVFHYAVOGDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDNKGETAHYAVOGDINSQVLQLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPIHSAKFESQKGCAMIISMDSSQIHSKDPYRGASPLHWAENA 300
DB 241 LCNARCNIMGPSGPFPIHTAMKFSQKGCAMIISMDSSQIHSKDPYRGASPLHWAENA 300

QY 301 RMLLRKGCNVNSTSAGNTALHVGVMRNFDCAIIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMRNFDCVIVLLTYGANAGTPEGHGNTPLHLAISK 360

QY	1	MOFFGRLVNTFGSVTNLFSNPRVKVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV	60
Db	1	MQFFGRLVNTFGSVTNLFSNPRVKVAVADYTSDDRVEEGQLILFQNTPNRTWDCVLV	60
QY	61	NPRNSQSGPRLFQLEADALVNFHQYSSQLLPYESSPQVLVHTEVLQHLTDLIRNHPSW	120
Db	61	NPRNSQSGPRLFQLEADALVNFHQYSSQLLPYESSPQVLVHTEVLQHLTDLIRNHPSW	120
QY	121	SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDGETLVELVOYCHTQMD	180
Db	121	SVAHLAVELGIRECFPHHSRIISCANCAENEGCTPLHLACRKGDGETLVELVOYCHTQMD	180
QY	181	VTDYKGETVFHYAVQDMSQVLLQGLGRNAVAGLVQVNNQGLTPHLACQLGKQEMVRVLL	240
Db	181	VTDYKGETVFHYAVQDMSQVLLQGLGRNAVAGLVQVNNQGLTPHLACQLGKQEMVRVLL	240
QY	241	LCNARCINMGPGYFIHSAKFSQKGCBAEMIISMDSSQIHSKDPYCASPLHWAKNAEMA	300
Db	241	LCNARCINMGPGYFIHSAKFSQKGCBAEMIISMDSSQIHSKDPYCASPLHWAKNAEMA	300
QY	301	RMLLKRCNCVNSTSSAGNTALHVGVMNRPFCAIVLLTHGANADARGEHNTPLHLSMSK	360
Db	301	RMLLKRCNCVNSTSSAGNTALHVGVMNRPFCAIVLLTHGANADARGEHNTPLHLSMSK	360
QY	361	DNVEMIKALIVFGAEVDTNPFGTPTFLASKIG	394
Db	361	DNVEMIKALIVFGAEVDTNPFGTPTFLASKIG	394

RESULT 8

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US-09-519-223-23
; Sequence 23, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-23

```

Query Match

100.0%; Score 2084; DB 3; Length 688;

Best Local Similarity 100.0%; Pred. No. 1.2e-222;		
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MQPFGRLVNTFGVGNLFSNPRFKVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV 60
Db	1	MQPFGRLVNTFGVGNLFSNPRFKVAVADYTSSDRVREGQLILFQNTPNRTWDCVLV 60
Qy	61	NPNRSQSGFLFQLELEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTLDIRNHPW 120
Db	61	NPNRSQSGFLFQLELEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTLDIRNHPW 120
Qy	121	SVAHLAVELGIRCFPHHSRIISCANCAENBEGCTPLHLACRKGDGELLVELVOYCHTQMD 180
Db	121	SVAHLAVELGIRCFPHHSRIISCANCAENBEGCTPLHLACRKGDGELLVELVOYCHTQMD 180
Qy	181	VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db	181	VTDYKGETVPHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Qy	241	LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300
Db	241	LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPRYGASPLHWAKNAEMA 300
Qy	301	RMLLKRGCVNNTSSAGNTALHVGVMNRNPFDCAI VLLTHGANADARGEHGNTPHLAMSK 360
Db	301	RMLLKRGCVNNTSSAGNTALHVGVMNRNPFDCAI VLLTHGANADARGEHGNTPHLAMSK 360
Qy	361	DNVEMI KALIVGAEDVTDPNDFGETPTFLASKIG 394
Db	361	DNVEMI KALIVGAEDVTDPNDFGETPTFLASKIG 394

RESULT 9

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US-09-927-180-23
: Sequence 23, Application US/09927180
: Patent NO. 6645736
: GENERAL INFORMATION:
: APPLICANT: Jones, Simon
: TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/927,180
: FILING DATE: 09-Aug-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/519,223
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 688 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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Db 1 MQFFGRLVNTFSVNTLFSNPNFRVKEVAVADYTSDDRVREBQQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHQYSSQLLPFYESSQVILHTEVLOHLTDLIRNHPSW 120
Db 61 NPNRSQSGFRLFOLEADALVNFHQYSSQLLPFYESSQVILHTEVLOHLTDLIRNHPSW 120
QY 121 SVAHLAVALGIRECFPHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVALGIRECFPHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 6
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 2084; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSVNTLFSNPNFRVKEVAVADYTSDDRVREBQQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTFSVNTLFSNPNFRVKEVAVADYTSDDRVREBQQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFOLEADALVNFHQYSSQLLPFYESSQVILHTEVLOHLTDLIRNHPSW 120
Db 61 NPNRSQSGFRLFOLEADALVNFHQYSSQLLPFYESSQVILHTEVLOHLTDLIRNHPSW 120
QY 121 SVAHLAVALGIRECFPHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVALGIRECFPHHSRIISCANCAENEBGCTPLHLACRKGDEIILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 7
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-23

Query Match 100.0%; Score 2084; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

Db 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBEGCTPLHLACRKGDGELVELVQYCHTQMD 180

Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBEGCTPLHLACRKGDGELVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

Db 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300

Db 241 LCNARCNINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300

QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGTPLHLAMSK 360

Db 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGTPLHLAMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDFGTPTFLASKIG 394

Db 361 DNVEMIKALIVFGAEVDTNDFGTPTFLASKIG 394

RESULT 4

US-08-555-568B-21

; Sequence 21, Application US/08555568B

; Patent No. 5976854

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/555,568B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 687 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-555-568B-21

Query Match 100.0%; Score 2084; DB 2; Length 687;

Best Local Similarity 100.0%; Pred. No. 1.2e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTTSSDRVREEGQLILFQNTPNRTWDCVLV 60

Db 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

Db 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBEGCTPLHLACRKGDGELVELVQYCHTQMD 180

Db 121 SVAHLAVELGIRECFPHHSRIISCANCAENEBEGCTPLHLACRKGDGELVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

Db 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300

Db 241 LCNARCNINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKNAEMA 300

QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGTPLHLAMSK 360

Db 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHGTPLHLAMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDFGTPTFLASKIG 394

Db 361 DNVEMIKALIVFGAEVDTNDFGTPTFLASKIG 394

RESULT 5

US-09-519-223-21

; Sequence 21, Application US/09519223

; Patent No. 6274140

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; APPLICANT: Tang, Jim

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/519,223

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/555,568

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 687 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-519-223-21

Query Match 100.0%; Score 2084; DB 3; Length 687;

Best Local Similarity 100.0%; Pred. No. 1.2e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFNPNFRVKEVAVADYTTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 2

US-09-519-223-17
; Sequence 17, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-17

Query Match 100.0%; Score 2084; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 5e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
DB 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
QY 61 NPNRSQSGRLFQLEADALVNFHOYSSQLLPFYESSQVLTHTVLOHLDLIRNHPSW 120

DB 61 NPNRSQSGRLFQLEADALVNFHOYSSQLLPFYESSQVLTHTVLOHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIIVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEIIVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVOGDINSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCNVNSTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 3

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 5e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:08:24 ; Search time 14.5289 Seconds
(without alignments)
2024.365 Million cell updates/sec

Title: US-10-612-668-17
Perfect score: 2084
Sequence: 1 MOFFGRLVNTFGVTLNFSN.....EVDTPNDGFTPTFLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2084	100.0	394	2	US-08-555-568B-17
2	2084	100.0	394	3	US-09-519-223-17
3	2084	100.0	394	4	US-09-927-180-17
4	2084	100.0	687	2	US-08-555-568B-21
5	2084	100.0	687	3	US-09-519-223-21
6	2084	100.0	687	4	US-09-927-180-21
7	2084	100.0	688	2	US-08-555-568B-23
8	2084	100.0	688	3	US-09-519-223-23
9	2084	100.0	688	4	US-09-927-180-23
10	2078	99.7	819	4	US-09-949-016-10948
11	1837	88.1	752	1	US-08-281-193-2
12	1837	88.1	752	1	US-08-422-106-2
13	1837	88.1	752	2	US-08-735-716-2
14	1837	88.1	752	2	US-08-555-568B-2
15	1837	88.1	752	3	US-09-519-223-2
16	1837	88.1	752	4	US-09-927-180-2
17	1837	88.1	752	5	PCT-US95-08069-2
18	494.5	23.7	896	4	US-09-270-767-46130
19	359.5	17.3	545	4	US-09-270-767-61684
20	338	16.2	843	2	US-09-172-977-3
21	338	16.2	843	3	US-09-104-108-3
22	332	15.9	1839	2	US-09-172-977-4
23	332	15.9	1839	4	US-09-404-108-4
24	332	15.9	2753	4	US-09-949-016-7659
25	332	15.9	2753	4	US-09-949-016-7660
26	332	15.9	3924	4	US-09-538-092-1246
27	305.5	14.7	1745	2	US-09-031-485-33

28	305.5	14.7	1745	2	US-08-847-429A-33	Sequence 33, Appl
29	305.5	14.7	1745	3	US-09-065-474-33	Sequence 33, Appl
30	305.5	14.7	1745	3	US-09-557-034-33	Sequence 33, Appl
31	301	14.4	786	4	US-09-509-802-2	Sequence 2, Appli
32	301	14.4	787	3	US-09-188-930-334	Sequence 334, App
33	301	14.4	787	4	US-09-312-283C-334	Sequence 334, App
34	296	14.2	1088	3	US-09-082-059-2	Sequence 2, Appli
35	296	14.2	3913	4	US-09-949-016-10933	Sequence 10933, A
36	296	14.2	4377	4	US-09-949-016-6978	Sequence 6978, Ap
37	294	14.1	1719	4	US-09-949-016-6966	Sequence 6966, Ap
38	294	14.1	1856	4	US-09-949-016-6964	Sequence 6964, Ap
39	294	14.1	1880	4	US-09-949-016-5876	Sequence 5876, Ap
40	294	14.1	1881	4	US-09-949-016-6965	Sequence 6965, Ap
41	294	14.1	1883	4	US-09-949-016-9010	Sequence 9010, Ap
42	294	14.1	1883	4	US-09-949-016-9011	Sequence 9011, Ap
43	294	14.1	1883	4	US-09-949-016-9012	Sequence 9012, Ap
44	294	14.1	1883	4	US-09-949-016-9013	Sequence 9013, Ap
45	294	14.1	1883	4	US-09-949-016-9014	Sequence 9014, Ap

ALIGNMENTS

RESULT 1
US-08-555-568B-17
; Sequence 17, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match	100.0%;	Score 2084;	DB 2;	Length 394;
Best Local Similarity	100.0%;	Pred. No. 5e-223;		
Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MOFFGRLVNTFGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60	
Db	1	MOFFGRLVNTFGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV	60	
QY	61	NPRNSGGRFLFQLEADALVNFHQYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPWS	120	
Db	61	NPRNSGGRFLFQLEADALVNFHQYSSQLLPFYESSPOVLHTEVLQHLTDLIRNHPWS	120	

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Search completed: May 26, 2005, 14:51:02
Job time : 61.7186 secs

Db	60	1	MQFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRBEGQLILFQNTPNRTWDCVLV	60
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Db	61	YPRNSQSGFRLFQLEADALVNFHQYSS	89	
Qy	121	SVANHLAVELGIRECFHHSRIISCANCAENBEGTPLHLACKRGDGEILVELVOYCHTQMD	180	
Db	90	-----	89	
Qy	181	VTDYKGETVFHYAVOGDNSQVLLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL	240	
Db	90	-----	101	
Qy	241	LCNARCNIMPNGYPIHSAKFQSGKCAEMIISMDSSQIHSKDPRYGASPLHWAKVAEMA	300	
Db	102	LCNARCNIMPNGYPIHSAKFQSGKCAEMIISMDSSQIHSKDPRYGASPLHWAKVAEMA	161	
Qy	301	RMLLKRGCVNSTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHGTPLHLAMSK	360	
Db	162	RMLLKRGCVNSTSSAGNTALHVAVMNRNRPDCAIVLLTHGANADARGEHGTPLHLAMSK	221	
Qy	361	DNVEMIKALIVFGAEVDPNDPFGTPTPLASKIG	394	
Db	222	DNVEMIKALIVFGAEVDPNDPFGTPTPLASKIG	255	

RESULT 6

US-10-108-260A-3237
; Sequence 3237, Application US/10108260A
; Publication No. US20040005560A1

```

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1

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Query Match	15.5%	Score 324;	DB 15;	Length 1330;
Best Local Similarity	27.0%;	Pred. No. 1.8e-21;		
Matches 99;	Conservative 62;	Mismatches 128;	Indels 77;	Gaps 9;

[illegible]

Qy	389	LASKIG	394
		:	
Db	647	LASQEG	652

RESULT 7

US-10-164-080-2
; Sequence 2, Application US/10164080
; Publication No. US20030087411A1

: GENERAL INFORMATION:
 : APPLICANT: BIRD, Timothy, A.
 : APPLICANT: HOGLAND, Pamela, M.
 : APPLICANT: PESCHON, Jacques, J.
 : APPLICANT: VIRCA, George, D.
 : TITLE OF INVENTION: DEATH ASSOCIATED KINASE
 : TITLE OF INVENTION: USE

Query Match	14.4%;	Score 301;	DB 14;	Length 786;
Best Local Similarity	31.8%;	Pred. No. 1.4e-19;		
Matches 92; Conservative	48;	Mismatches 137;	Indels 12;	Gaps 8;

171 Y WAYCUEAMVITVYVCEMUEIVVVO CONSCUT OT T CENAVVOT NOIVNVOY EBY IIT XCO 330

Y 171 LVQYCHTQMDVTDYKGETVFHYAVQ-GDNSQVLQLLGRNAVAGLNQVNNQGLTFLHLACQ 229

[illegible]

230 LGKQEMVRVLLLCNARCNIIMPNGY-PIHSAMKFSQKGCAEMIISMDSQIHSKDPRYGA 288

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289 SPLHWAK---NAEMARMLLKRGCVNSTSSAGNTALHVGVMRNRFDCAI V L L T H G A N A D A 345

346 RGEHGNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 8

S-10-299-327-2
Sequence 2, Application US/10299327
Publication No. US20030104482A1

GENERAL INFORMATION: 020605010746ZAL
APPLICANT: Immunex Corp.
APPLICANT: Bird, Timothy
APPLICANT: Virca, G.D.
TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
FILE REFERENCE: 2899-115

```

;
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 2084; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
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DB 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIG 394

RESULT 4
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TANG, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/519,223
;
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 688 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 2084; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-190;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
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DB 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIG 394

RESULT 5
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 59.2%; Score 1234.5; DB 15; Length 667;
Best Local Similarity 64.0%; Pred. No. 3.2e-109;
Matches 252; Conservative 1; Mismatches 2; Indels 139; Gaps 1;

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DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
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DB 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIG 393
DB 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIG 393

RESULT 5
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 59.2%; Score 1234.5; DB 15; Length 667;
Best Local Similarity 64.0%; Pred. No. 3.2e-109;
Matches 252; Conservative 1; Mismatches 2; Indels 139; Gaps 1;

QY 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRGDGEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDINSQVLQLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNYPITHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTFNDGETPTFLASKIG 394

RESULT 5
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 59.2%; Score 1234.5; DB 15; Length 667;
Best Local Similarity 64.0%; Pred. No. 3.2e-109;
Matches 252; Conservative 1; Mismatches 2; Indels 139; Gaps 1;

QY 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVNTLFSNPRVKEVAVADYTSDDRVRREGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFOLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTDLIRNHPWS 12
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LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.1e-191;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPITHSAMKFSQKGCAMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGYPITHSAMKFSQKGCAMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 2
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 2084; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
DB 61 NPNRSQSGFRLFQLEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
QY 121 SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFPHHSRIISCANCAENEEGCTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIIMPNGYPITHSAMKFSQKGCAMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGYPITHSAMKFSQKGCAMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 3
US-09-927-180-23
; Sequence 23, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:20:02 ; Search time 53.7186 Seconds
(without alignments)
2530.207 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MOFFRLVNTSGVTNLFSEN.....EVDTPNDFGTPTFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_PUB_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2084	100.0	394	9	US-09-927-180-17
2	2084	100.0	687	9	US-09-927-180-21
3	2084	100.0	688	9	US-09-927-180-23
4	1837	88.1	752	9	US-09-927-180-2
5	1234.5	59.2	667	15	US-10-108-260A-3778
6	324	15.5	1330	15	US-10-108-260A-3237
7	301	14.4	786	14	US-10-164-080-2
8	301	14.4	786	14	US-10-299-327-2
9	301	14.4	786	14	US-10-128-174-13
10	301	14.4	786	14	US-10-128-174-31
11	301	14.4	786	14	US-10-128-174-32
12	301	14.4	786	14	US-10-128-174-33
13	301	14.4	787	10	US-09-866-050A-334

14	300.5	14.4	347	14	US-10-128-174-30	Sequence 30, Appl
15	300.5	14.4	1724	9	US-09-964-899-43	Sequence 43, Appl
16	296	14.2	1094	17	US-10-479-764-22	Sequence 22, Appl
17	296	14.2	3913	15	US-10-334-143-45	Sequence 45, Appl
18	288	13.8	1762	14	US-10-205-194-117	Sequence 117, Appl
19	283.5	13.6	784	14	US-10-164-080-7	Sequence 7, Appl
20	283.5	13.6	784	15	US-10-258-951-70	Sequence 70, Appl
21	281.5	13.5	784	14	US-10-354-358-38	Sequence 38, Appl
22	281.5	13.5	784	14	US-10-128-174-12	Sequence 12, Appl
23	281.5	13.5	784	15	US-10-658-904-2	Sequence 2, Appl
24	280.5	13.5	720	15	US-10-433-794-20	Sequence 20, Appl
25	280.5	13.5	765	14	US-10-128-174-3	Sequence 3, Appl
26	280.5	13.5	765	14	US-10-128-174-34	Sequence 34, Appl
27	280.5	13.5	765	14	US-10-128-174-35	Sequence 35, Appl
28	280.5	13.5	765	14	US-10-128-174-36	Sequence 36, Appl
29	280.5	13.5	765	14	US-10-128-174-37	Sequence 37, Appl
30	280.5	13.5	765	14	US-10-128-174-38	Sequence 38, Appl
31	280.5	13.5	765	14	US-10-128-174-39	Sequence 39, Appl
32	280.5	13.5	765	14	US-10-128-174-40	Sequence 40, Appl
33	280.5	13.5	765	14	US-10-128-174-41	Sequence 41, Appl
34	280.5	13.5	765	14	US-10-128-174-42	Sequence 42, Appl
35	280.5	13.5	765	14	US-10-128-174-43	Sequence 43, Appl
36	280.5	13.5	765	14	US-10-128-174-44	Sequence 44, Appl
37	280.5	13.5	765	15	US-10-182-243-56	Sequence 56, Appl
38	278.5	13.4	784	16	US-10-648-593-153	Sequence 153, Appl
39	272	13.1	367	15	US-10-250-613-6	Sequence 6, Appl
40	272	13.1	994	17	US-10-717-665-38	Sequence 38, Appl
41	272	13.1	1056	17	US-10-479-764-18	Sequence 18, Appl
42	271.5	13.0	1053	15	US-10-291-172-343	Sequence 343, Appl
43	271.5	13.0	1053	15	US-10-221-278-343	Sequence 343, Appl
44	267.5	12.8	919	15	US-10-108-260A-4122	Sequence 4122, Ap
45	258	12.4	1023	15	US-10-369-493-6689	Sequence 6689, Ap

ALIGNMENTS

RESULT 1

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
;

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Search completed: May 26, 2005, 14:13:49
Job time : 60.101 secs

Best Local Similarity 87.3%; Pred. No. 1.1e-191; Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;		phospholipids. The invention provides a process for producing such an enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence of one or more amino acid sequences selected from AAW01480-92. cPLA2/B has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-arachidonyl- phosphatidylcholine. The enzyme is useful for screening anti-inflammatory agents mediated by the arachidonic acid cascade, for treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF field.)	
QY	1 MOFFGRLVNTFSQVTLNFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60	CC	Sequence 752 AA;
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Db	61 SPNPHSGFRLFQLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW 120	CC	Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
QY	121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSGILVELVOYCHTQMD 180	QY	1 MOFFGRLVNTFSQVTLNFSNPRVKEVAVADYTSSDRVREEGQLILFQNTNRTWDCVLV 60
Db	121 TVTHLAVELGIRECFHHSRIISCANSTENEBCGCTPLHLACRKGDSILVELVOYCHAQMD 180	Db	1 MOFFGRLVNTLSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY	181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240	QY	61 NPNRSQSGFRLFQLELEADALVNFHQYSQQLPPFYESSQVLHTEVLOHLTDLIRNHPSW 120
Db	181 VTDNKGETAFAHYAVQGDNSQVLQLGKNASAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240	Db	61 SPNPHSGFRLFQLESEADALVNFQFSSQLPPFYESSQVLHVEVLQHLSDLIRSHPSW 120
QY	241 LCNARCNIMGNGYPITHAMKFSQKCAEMIISMDSQIHSKDPRIYAGSPPLHWAKNAEMA 300	QY	121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSGILVELVOYCHTQMD 180
Db	241 LCNARCNVMGSPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPRIYAGSPPLHWAKNAEMA 300	Db	121 TVTHLAVELGIRECFHHSRIISCANSTENEBCGCTPLHLACRKGDSILVELVOYCHAQMD 180
QY	301 RMLLKRGCVNNTSSAGNTALHVGVMNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360	QY	181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
Db	301 RMLLKRGCDVDSTSAAGNTALHVAVMNRNRFDCVMVLLTYGANAGTPEGHGNTPLHLAISK 360	Db	181 VTDNKGETAFAHYAVQGDNSQVLQLGKNASAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY	361 DNVEMIKALIVFGAEVDTNDGGETPTFLASKI 393	QY	241 LCNARCNIMGNGYPITHAMKFSQKCAEMIISMDSQIHSKDPRIYAGSPPLHWAKNAEMA 300
Db	361 DNMEMIKALIVFGAEVDTNDGGETPAFMASKI 393	Db	241 LCNARCNVMGSPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPRIYAGSPPLHWAKNAEMA 300
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DT	12-FEB-1997 (first entry)	Db	361 DNMEMIKALIVFGAEVDTNDGGETPAFMASKI 393
XX	Calcium-independent cytosolic phospholipase A2/B.	RESULT 14 AAW13163 ID AAW13163 standard; protein; 752 AA.	
XX	cPLA2/B; calcium-independent cytosolic phospholipase A2/B;	XX	AAW13163;
KW	arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;	DT	17-OCT-2003 (revised)
KW	anti-inflammatory; screen; rheumatoid arthritis.	DT	25-MAR-2003 (revised)
OS	Synthetic.	DT	20-MAY-1997 (first entry)
XX	US5554511-A.	DE	Ca-independent phospholipase A2/B protein.
XX	10-SEP-1996.	XX	Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
XX	14-APR-1995; 95US-00422420.	KW	Chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
XX	27-JUL-1994; 94US-00281193.	KW	Heparin Toyopearl; chromatofocussing; eukaryotic expression vector; COS;
XX	(GEMY) GENETICS INST INC.	KW	CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.
PI	Tang J, Jones S;	OS	Cricetulus griseus; ovary cells.
DR	WPI; 1996-424653/42.	XX	US5589170-A.
XX	N-PSDB; AAT44578.	XX	31-DEC-1996.
PT	Prod. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing	XX	14-APR-1995; 95US-00422106.
PT	host cells contg. the phospholipase gene, useful for screening anti-	XX	27-JUL-1994; 94US-00281193.
PT	inflammatory agents for treating e.g. rheumatoid arthritis.	XX	(GEMY) GENETICS INST INC.
PS	Claim 1; Col 15-22; 24pp; English.	XX	
CC	The present sequence is that of a calcium-independent cytosolic	XX	
CC	phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release	XX	
CC	of arachidonic acid in specific tissues characterised by unique membrane	XX	

AC ABM84354;
DT 18-NOV-2004 (first entry)
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4603.
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
OS WO2004023973-A2.
XX 25-MAR-2004.
PN 12-SEP-2003; 2003WO-US028227.
PD 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
PA (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX WPI: 2004-329368/30.
DR N-PSDB; ACM43006.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorders, developmental disorders, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 810 AA;

Query Match 98.6%; Score 2054; DB 8; Length 810;
Best Local Similarity 93.1%; Pred. No. 1.7e-215;
Matches 393; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MOFFGLVNTFSGVTNLFNPNFRVKEVAVADYTSSDRVREGQLILFQNTNRTWDCVLV 60
DB 1 MOFFGLVNTFSGVTNLFNPNFRVKEVAVADYTSSDRVREGQLILFQNTNRTWDCVLV 60
QY 61 NPNRSQSGFRLPQLEADALVNFHQYSSQLLPFFYESSPQVLHTEVQLHTDLIRNPSW 120
DB 61 NPNRSQSGFRLPQLEADALVNFHQYSSQLLPFFYESSPQVLHTEVQLHTDLIRNPSW 120
QY 121 SVAHLAVELGIRECPHHSRII-----SCANCAENREG 152
DB 121 SVAHLAVELGIRECPHHSRII-----SCANCAENREG 152

DB 121 SVAHLAVELGIRECPHHSRII-----SCANCAENREG 180
QY 153 CTPLHLACRKGDEILVELVOYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 212
DB 181 CTPLHLACRKGDEILVELVOYCHTQMDVTDYKGETVFHYAVQGDNSQVLQLGRNAVAG 240
QY 213 LNOVNNQGLTPLHLACQLGQEMVRVLLLCNARCINMGPNGYPIHSAMKFSQKCAEMII 272
DB 241 LNOVNNQGLTPLHLACQLGQEMVRVLLLCNARCINMGPNGYPIHSAMKFSQKCAEMII 300
QY 273 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLKRCNCNVNSTSSAGNTALHVGVMNRFD 332
DB 301 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLKRCNCNVNSTSSAGNTALHVGVMNRFD 360
QY 333 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDFGPTPTFLASK 392
DB 361 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDFGPTPTFLASK 420
QY 393 IG 394
DB 421 IG 422

RESULT 12
AAR83018
ID AAR83018 standard; protein; 752 AA.
AC AAR83018;
XX 15-JUN-1996 (first entry)
XX Calcium-independent cytosolic phospholipase-A2/B enzyme.
KW CHO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
KW phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
KW antibody.
XX Cricetulus griseus.
XX US5466595-A.
XX 14-NOV-1995.
XX 27-JUL-1994; 94US-00281193.
XX 27-JUL-1994; 94US-00281193.
XX (GEMY) GENETICS INST INC.
XX Tang J, Jones S;
XX WPI; 1996-009526/01.
XX N-PSDB; AAT05842.
XX Isolated polynucleotide encoding cytosolic phospholipase A2/B - for
PT producing enzyme for use in screening anti-inflammatory agents and prodn.
PT of antibodies.
XX Claim 5; Col 15-22; 24pp; English.
XX The enzyme may be produced recombinantly in host cells such as animal
CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
CC protein is used to screen for agents which inhibit phospholipase activity
CC for use as antiinflammatory agents. These agents can be used to treat
CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
CC and other disease mediated by increased levels of prostaglandins,
CC leukotriene or platelet activating factor. The enzyme can also be used
CC for the production of antibodies for use as research or diagnostic tools
XX
SQ Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;

CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX
SQ Sequence 806 AA;

Query Match 99.7%; Score 2078; DB 8; Length 806;
Best Local Similarity 99.7%; Pred. No. 4e-218; 1; Indels 0; Gaps 0;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCNIIMPNGYPPIHSAMKFSQKGCABMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGYPPIHSAMKFSQKGCABMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLRGCGNVNTSSAGNTALHVGWNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCGNVNTSSAGNTALHVGWNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIG 394
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIG 394

RESULT 10
ABM84355
ID ABM84355 standard; protein; 810 AA.
XX
AC ABM84355;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4604.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
FN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney BW, Deleagane AM, Panesar IS, Banville SC, Reddy IP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI: 2004-329368/30.
DR N-PSDB; ACN43007.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 810 AA;

Query Match 98.6%; Score 2054; DB 8; Length 810;
Best Local Similarity 93.1%; Pred. No. 1.7e-215; 1; Indels 28; Gaps 1;
Matches 393; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW 120
DB 61 NPRNSQSGFRLFQLELEADALVNFHQYSSQLLPFYESSQVLHTEVLQHLTDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 152
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 152

QY 153 CTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQGRNAVAG 212
DB 181 CTPLHLACRKGDEILVELVQYCHTQMDVTDYKGETVFHYAVQGDNSQVLQGRNAVAG 240

QY 213 LNVNNOGLTPLHLACOLGKQEMVRVLLCNARCNIIMPNGYPPIHSAMKFSQKGCABMI 272
DB 241 LNVNNOGLTPLHLACOLGKQEMVRVLLCNARCNIIMPNGYPPIHSAMKFSQKGCABMI 300

QY 273 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLRGCGNVNTSSAGNTALHVGWNRNFD 332
DB 301 SMDSSQIHSKDPYRGASPLHWAKNAEMARMLLRGCGNVNTSSAGNTALHVGWNRNFD 360

QY 333 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDFGETPTFLASK 392
DB 361 AIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTNDFGETPTFLASK 420

QY 393 IG 394
DB 421 IG 422

RESULT 11
ABM84354
ID ABM84354 standard; protein; 810 AA.
XX

PS	Claim 6; Page 28-30; 41pp; English.	
XX	The invention relates to a purified mammalian calcium independent	
CC	cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is	
CC	characterized by activity in the absence of calcium and has a molecular	
CC	weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified	
CC	calcium independent phospholipase enzyme is useful for identifying an	
CC	inhibitor of phospholipase activity which involves combining (I),	
CC	phospholipid and candidate inhibitor compound, and observing whether the	
CC	enzyme cleaves the phospholipid and releases fatty acid from it. A	
CC	pharmaceutical composition (PC) comprising a therapeutically effective	
CC	amount of the inhibitor is useful for reducing inflammation and for	
CC	treating inflammatory conditions including rheumatoid arthritis,	
CC	psoriasis, asthma, inflammatory bowel disease and other diseases mediated	
CC	by increased levels of prostaglandins, leukotriene or platelet activating	
CC	factor. A composition comprising an antibody which binds to (I) is useful	
CC	as research and diagnostic tool, and is also useful in the study of	
CC	phospholipase A2 activity and inflammatory conditions. The present	
CC	sequence represents a human cPLA2/B enzyme longer splice variant (clone	
CC	19b)	
XX		
SQ	Sequence 688 AA;	
	Query Match 100.0%; Score 2084; DB 5; Length 688;	
	Best Local Similarity 100.0%; Pred. No. 6.8e-219;	
	Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MQFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
Db	1 MQFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
QY	61 NPNRSQSGFRLPQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTDLIRNHPWS 120	
Db	61 NPNRSQSGFRLPQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTDLIRNHPWS 120	
QY	121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGIELVELVQYCHTQMD 180	
Db	121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGIELVELVQYCHTQMD 180	
QY	181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240	
Db	181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240	
QY	241 LCNARCNIMGPNGYPIHLSAMKFSQKCAEMIISMDSQIHSKDPRIAGSPLHWAKNAEMA 300	
Db	241 LCNARCNIMGPNGYPIHLSAMKFSQKCAEMIISMDSQIHSKDPRIAGSPLHWAKNAEMA 300	
QY	301 RMLLKRGCVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360	
Db	301 RMLLKRGCVNSTSSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360	
QY	361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394	
Db	361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394	
RESULT 7		
ADD93407		
ID	ADD93407 standard; protein; 784 AA.	
XX		
AC	ADD93407;	
XX		
DT	29-JAN-2004 (first entry)	
XX	Human lipid-associated molecule LIPAM-14 polypeptide.	
DE		
XX	Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;	
KW	antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;	
KW	antiinflammatory; thyromimetic; antiallergic; cerebroprotective;	
KW	gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;	
KW	antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;	
KW	virucide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;	
KW	nootropic.	
XX		

XX	Homo sapiens.	
OS	WO2003083081-A2.	
XX		
PN	09-OCT-2003.	
XX		
PD	27-MAR-2003; 2003WO-US009755.	
XX		
PF	29-MAR-2002; 2002US-0368722P.	
XX		
PR	03-MAY-2002; 2002US-0377576P.	
PR	05-JUL-2002; 2002US-0393934P.	
PR	27-SEP-2002; 2002US-0414269P.	
XX	(INCV-) INCVTE CORP.	
PA		
XX	Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;	
PI	Baughn MR, Lee SA, Griffin JA, Kabie AE, Elliott VS, Chang H;	
PI	Lee S, Rankumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;	
PI	Jackson AA;	
XX		
WPI	2003-788347/74.	
DR	N-PSDB; ADD93426.	
XX		
XX	New LIPAM polypeptides, useful for diagnosing, preventing, and treating	
PT	disorders associated with abnormal expression or activity of LIPAM, e.g.	
PT	neuromuscular, immunological, cardiovascular disorders, cancer and/or	
PT	infections.	
XX		
PS	Claim 69; Page 206-207; 238pp; English.	
XX		
CC	The present sequence is the protein sequence of human lipid-associated	
CC	molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows	
CC	homology to human Ca ²⁺ -independent phospholipase A2 short isoform. This	
CC	is one of 19 LIPAM polypeptides of the invention. The invention relates	
CC	to these novel LIPAMs and the nucleic acids encoding them, and to the use	
CC	of nucleic acids and proteins in the diagnosis, treatment and prevention	
CC	of disorders associated with abnormal expression or activity of LIPAM	
CC	such as neurodegenerative disorders (e.g. Parkinson's disease,	
CC	Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,	
CC	catatonica), endocrine disorders (e.g. diabetes, Grave's disease), cancers	
CC	(e.g. leukemia, cervical or breast cancers), immunological disorders	
CC	(e.g. scleroderma, systemic lupus erythematosus, allergies),	
CC	gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.	
CC	Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,	
CC	parasitic, protozoal, helminthic), cardiovascular disorders (e.g.	
CC	atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention	
CC	also relates to the assessment of the effects of exogenous compounds on	
CC	the expression of nucleic acids and LIPAMs. The invention provides	
CC	expression vectors, host cells, antibodies, agonists and antagonists,	
CC	transgenic organisms, and arrays and microarrays of the polynucleotides.	
XX		
SQ	Sequence 784 AA;	
	Query Match 99.7%; Score 2078; DB 7; Length 784;	
	Best Local Similarity 99.7%; Pred. No. 3.8e-218;	
	Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MQFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60	
Db	33 MQFFGRLVNTFSGVTNLFNSNPRFRKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 92	
QY	61 NPNRSQSGFRLPQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTDLIRNHPWS 120	
Db	93 NPNRSQSGFRLPQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTDLIRNHPWS 152	
QY	121 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGIELVELVQYCHTQMD 180	
Db	153 SVAHLAVELGIRECFPHHSRIISCANCAENEECTPLHLACRKGDDGIELVELVQYCHTQMD 212	
QY	181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240	
Db	213 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 272	

QY 121 SVAHLAVELGIRECFHSHRSIIISCANCAENEECTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHRSIIISCANCAENEECTPLHLACRKGDEIILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCINMGPNPGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCINMGPNPGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
DB 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 5

AAW17848
ID AAW17848 standard; protein; 688 AA.
AC AAW17848;
XX

DT 07-AUG-1997 (first entry)
XX

DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
XX

KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX inflammation; inhibitor; antiinflammatory.
KW

OS Homo sapiens.
XX

PN WO9717448-A2.
XX

PD 15-MAY-1997.
XX

PF 07-NOV-1996; 96WO-US017794.
XX

PR 08-NOV-1995; 95US-00555568.
XX

XX (GENY) GENETICS INST INC.
PA

PI Jones S, Tang J;
XX

DR WPI: 1997-281037/25.
XX

DR N-PSDB; AAT68826.
XX

XX Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.
XX

PS Claim 12; Page 54-56; 74pp; English.
XX

CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is characterised by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839-44). It is an alternatively spliced variant of another isolated polypeptide (AAW17846) and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade
CC

XX Sequence 688 AA;
SQ

Query Match 100.0%; Score 2084; DB 2; Length 688;
X

Best Local Similarity 100.0%; Pred. No. 6.8e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVTNLFSPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60
DB 1 MOFFGRLVNTSGVTNLFSPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVILV 60

QY 61 NPNRSQSGFRLLFQLELEADALVNFHQYSSQLLPFYESSQVILHTEVLOHLDLIRNHPSW 120
DB 61 NPNRSQSGFRLLFQLELEADALVNFHQYSSQLLPFYESSQVILHTEVLOHLDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHSHRSIIISCANCAENEECTPLHLACRKGDEIILVELVOYCHTQMD 180
DB 121 SVAHLAVELGIRECFHSHRSIIISCANCAENEECTPLHLACRKGDEIILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNVNNOGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCINMGPNPGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCINMGPNPGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360
DB 301 RMLLRGCNVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHGNTPHLHMSK 360

QY 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDGFTPTFLASKIG 394

RESULT 6

ABB82232
ID ABB82232 standard; protein; 688 AA.
XX

AC ABB82232;
XX

DT 08-JAN-2003 (first entry)
XX

DE Human cPLA2/B splice variant (clone 19b).
XX

KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX antiasthmatic; human.
KW

OS Homo sapiens.
XX

PN US2002106364-A1.
XX

PD 08-AUG-2002.
XX

PF 09-AUG-2001; 2001US-00927180.
XX

PR 27-JUL-1994; 94US-00281193.
XX

PR 14-APR-1995; 95US-00422106.
XX

PR 14-APR-1995; 95US-00422420.
XX

PR 26-JUN-1995; 95WO-US008069.
XX

PR 08-NOV-1995; 95US-00555568.
XX

PR 09-SEP-1998; 98US-00149988.
XX

PR 06-MAR-2000; 2000US-00519223.
XX

XX (GENY) GENETICS INST INC.
PA

PI Jones S, Tang J;
XX

DR WPI: 2002-739923/80.
XX

DR N-PSDB; ABV73011.
XX

XX Novel composition comprising purified mammalian calcium independent phospholipase enzyme, useful for the screening of inhibitors of phospholipase activity, is active in the absence of calcium.
PT

```
XX PN WO9717448-A2.
XX PD 15-MAY-1997.
XX PF 07-NOV-1996; 96WO-US017794.
XX PR 08-NOV-1995; 95US-00555568.
XX PA (GEMY ) GENETICS INST INC.
XX PI Jones S, Tang J;
XX PD WPI; 1997-281037/25.
XX DR N-PSDB; AAT68825.
XX PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX PT mammalian subject.
XX PS Claim 12; Page 49-51; 74pp; English.
XX CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
XX CC characterised by activity in the absence of calcium, by activity in a
XX CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
XX CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
XX CC lack of stimulation by ATP, and by including in its sequence at least one
XX CC of the amino acid sequences given in AAW17839- 44). It is an
XX CC alternatively spliced variant of another isolated polypeptide (AAW17845)
XX CC and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes
XX CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
XX CC thought to be involved in the release of arachidonic acid in specific
XX CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
XX CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
XX CC drugs which inhibit the arachidonic acid cascade
XX SQ Sequence 687 AA;
Query Match 100.0%; Score 2084; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 6.8e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWS 120
QY 121 SVANHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDBILVELVQYCHTQMD 180
DB 121 SVANHLAVELGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDBILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVQNNQGLTPLHLACQLGQKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVQNNQGLTPLHLACQLGQKQEMVRVLL 240
QY 241 LCNARCNIIMPNGPYTHSAMKFSQKCAEMIISMDSQHSQKDPKRYGASPLHWAKNAEMA 300
DB 241 LCNARCNIIMPNGPYTHSAMKFSQKCAEMIISMDSQHSQKDPKRYGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNNVNTSSAGNTALHGVNMRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNNVNTSSAGNTALHGVNMRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDFTGFTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDFTGFTPTFLASKIG 394
RESULT 4
ABB82231
ID ABB82231 standard; protein; 687 AA.
```

```
XX ABB82231;
XX AC
XX DT 08-JAN-2003 (first entry)
XX DE Human cPLA2/B splice variant (clone 19a).
XX XX
XX KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX KW antiasthmatic; human.
XX OS Homo sapiens.
XX XX
XX PN US2002106364-A1.
XX PD 08-AUG-2002.
XX PF 09-AUG-2001; 2001US-00927180.
XX PR 27-JUL-1994; 94US-00281193.
XX PR 14-APR-1995; 95US-00422106.
XX PR 14-APR-1995; 95US-00422420.
XX PR 26-JUN-1995; 95WO-US008069.
XX PR 08-NOV-1995; 95US-00555568.
XX PR 09-SEP-1998; 98US-00149988.
XX PR 06-MAR-2000; 2000US-00519223.
XX PA (GEMY ) GENETICS INST INC.
XX XX
XX PI Jones S, Tang J;
XX XX
XX DR WPI; 2002-739923/80.
XX DR N-PSDB; ABV73010.
XX PT Novel composition comprising purified mammalian calcium independent
XX PT phospholipase enzyme, useful for the screening of inhibitors of
XX PT phospholipase activity, is active in the absence of calcium.
XX PS Claim 6; Page 23-25; 41pp; English.
XX CC The invention relates to a purified mammalian calcium independent
XX CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
XX CC characterized by activity in the absence of calcium and has a molecular
XX CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
XX CC calcium independent phospholipase enzyme is useful for identifying an
XX CC inhibitor of phospholipase activity which involves combining (I),
XX CC phospholipid and candidate inhibitor compound, and observing whether the
XX CC enzyme cleaves the phospholipid and releases fatty acid from it. A
XX CC pharmaceutical composition (PC) comprising a therapeutically effective
XX CC amount of the inhibitor is useful for reducing inflammation and for
XX CC treating inflammatory conditions including rheumatoid arthritis,
XX CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
XX CC by increased levels of prostaglandins, leukotriene or platelet activating
XX CC factor. A composition comprising an antibody which binds to (I) is useful
XX CC as research and diagnostic tool, and is also useful in the study of
XX CC phospholipase A2 activity and inflammatory conditions. The present
XX CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
XX CC 19a)
XX SQ Sequence 687 AA;
Query Match 100.0%; Score 2084; DB 5; Length 687;
Best Local Similarity 100.0%; Pred. No. 6.8e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWS 120
DB 61 NPNRSQSGRLFQLELEADALVNFHQYSSQLLPFFYESSQVLTVEVLQHLTDLIRNHPWS 120
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XX Sequence 394 AA;
SQ Query Match
    Best Local Similarity 100.0%; Score 2084; DB 2; Length 394;
    Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPFYESSQVLTHTVQLHTDILRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPFYESSQVLTHTVQLHTDILRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIG 394

RESULT 2
ABB82229
ID ABB82229 standard; protein; 394 AA.
AC ABB82229;
XX
XX 08-JAN-2003 (first entry)
XX Calcium independent phospholipase A2/B (cPLA2/B) (clone 19a).
XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
XX antiasthmatic; human.
XX Homo sapiens.
XX US2002106364-A1.
XX
XX 08-AUG-2002.
XX
XX 09-AUG-2001; 2001US-00927180.
XX
XX 27-JUL-1994; 94US-00281193.
XX 14-APR-1995; 95US-00422106.
XX 14-APR-1995; 95US-00422420.
XX 26-JUN-1995; 95WO-00080069.
XX 08-NOV-1995; 95US-00555568.
XX 09-SEP-1998; 98US-00149988.
XX 06-MAR-2000; 2000US-00519223.
XX (GENY ) GENETICS INST INC.
XX
XX Jones S, Tang J;
XX WPI: 2002-739923/80.
XX N-PSDB; ABV73008.
XX
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```
PT Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.
PS Claim 6; Page 18-19; 41pp; English.
XX
XX The invention relates to a purified mammalian calcium independent
XX cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
XX characterized by activity in the absence of calcium and has a molecular
XX weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
XX calcium independent phospholipase enzyme is useful for identifying an
XX inhibitor of phospholipase activity which involves combining (I),
XX phospholipid and candidate inhibitor compound, and observing whether the
XX enzyme cleaves the phospholipid and releases fatty acid from it. A
XX pharmaceutical composition (PC) comprising a therapeutically effective
XX amount of the inhibitor is useful for reducing inflammation and for
XX treating inflammatory conditions including rheumatoid arthritis,
XX psoriasis, asthma, inflammatory bowel disease and other diseases mediated
XX by increased levels of prostaglandins, leukotriene or platelet activating
XX factor. A composition comprising an antibody which binds to (I) is useful
XX as research and diagnostic tool, and is also useful in the study of
XX phospholipase A2 activity and inflammatory conditions. The present
XX sequence represents a human cPLA2/B enzyme (clone 19a)
XX Sequence 394 AA;
SQ Query Match
    Best Local Similarity 100.0%; Score 2084; DB 5; Length 394;
    Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPFYESSQVLTHTVQLHTDILRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLPFYESSQVLTHTVQLHTDILRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
DB 241 LCNARCNIIMGPNGYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEWA 300
QY 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360
DB 301 RMLLKRGCVNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGHGNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNDPFGTPTFLASKIG 394

RESULT 3
AAW17847
ID AAW17847 standard; protein; 687 AA.
XX
XX AAW17847;
XX
XX 07-AUG-1997 (first entry)
XX Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX inflammation; inhibitor; antiinflammatory.
XX Homo sapiens.
XX
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:05:39 ; Search time 50.851 Seconds

(without alignments)
2996.666 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MQGRLVNTFSGVNLFNS.....EVDTFNFGTPTFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_l6Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2084	100.0	394	2	AAW17845	Cytosolic
2	2084	100.0	394	5	ABB82229	Calcium i
3	2084	100.0	687	2	AAW17847	Cytosolic
4	2084	100.0	687	5	ABB82231	Human CPL
5	2084	100.0	688	2	AAW17848	Cytosolic
6	2084	100.0	688	5	ABB82232	Human CPL
7	2078	99.7	784	7	ADD93407	Human lip
8	2078	99.7	806	5	AAE25968	Human PLA
9	2078	99.7	806	8	AD019776	Human PRO
10	2054	98.6	810	8	ABM84355	Human dia
11	2054	98.6	810	8	ABM84354	Human dia
12	1837	88.1	752	2	AAW01479	Calcium-i
13	1837	88.1	752	2	AAW01479	Calcium-i
14	1837	88.1	752	2	AAW13163	Ca-indepe
15	1837	88.1	752	2	AAW17849	Hamster c
16	1837	88.1	752	2	AAW81825	Chinese h
17	1837	88.1	752	5	ABB82215	Calcium i
18	1808.5	86.8	751	7	ADDA46244	Rat Prote
19	1808.5	86.8	751	7	ADBE60532	Rat Prote
20	1808.5	86.8	751	7	ADBE5230	Rat Prote
21	1808.5	86.8	751	7	ADBE60536	Rat Prote
22	1234.5	59.2	667	7	ADM05093	Human pro
23	836	40.1	401	4	AAB92811	Human pro
24	494.5	23.7	877	4	ABB62624	Drosophil
25	338	16.2	843	7	ADD27861	Rat ankyr

ALIGNMENTS

RESULT 1

AAW17845

ID AAW17845 standard; protein; 394 AA.

XX

AC AAW17845;

XX

DT 07-AUG-1997 (first entry)

XX Cytosolic phospholipase A2/B (clone 19a product).

DE Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

XX inflammation; inhibitor; antiinflammatory.

KW Homo sapiens.

OS WO9717448-A2.

XX 15-MAY-1997.

PD 07-NOV-1996; 96WO-US017794.

PF 08-NOV-1995; 95US-00555568.

XX (GEMY) GENETICS INST INC.

XX Jones S, Tang J;

XX WPI; 1997-281037/25.

DR N-PSDB; AAT68823.

XX Calcium independent phospholipase A2/B - used to reduce inflammation in a

PT mammalian subject.

XX Claim 12; Page 43-44; 74pp; English.

PS A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is

XX characterised by activity in the absence of calcium, by activity in a

CC mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-

CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a

CC lack of stimulation by ATP, and by including in its sequence at least one

CC of the amino acid sequences given in AAW17839- 44). It is encoded by

CC partial cDNA clone 19a (AAT68823), derived from Burkitt's lymphoma Raji

CC (ATCC CRL86) cells. Other PLA2/B enzymes (AAW17846-48) have also been

CC identified. sPLA2/B enzymes are thought to be involved in the release of

CC arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides

CC produced in transformed host cells can be used to screen for sPLA2/B

CC inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic

CC acid cascade

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FT	REPEAT	1939	1950	Repeat A.
FT	DOMAIN	3536	3620	Death.
FT	VARSP LIC	1039	1039	Q -> QFLGKJHLPTAPPPLNEGESIVSRILQLGPPGTK (in isoform 2).
FT	VARSP LIC	1444	3528	/FTid=VSP_000267. Missing (in isoform 2 and isoform 3).
FT	CONFLICT	475	476	/FTid=VSP_000268. GQ -> PE (in Ref. 4).
FT	CONFLICT	971	971	I -> S (in Ref. 1).
FT	CONFLICT	3581	3582	OY -> HA (in Ref. 1).
FT	CONFLICT	3586	3586	I -> Y (in Ref. 1).
SQ	SEQUENCE	3924	AA; 430337 MW; 52AC496C428E29D2 CRC64;	

Query Match

Best Local Similarity 15.9%; Score 332; DB 1; Length 3924;

Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;

QY	103	HTEVLQHLTD	-----LIRNHPWSVAHLAVELGIRECFHH-----SRIL 141
Db	311	HQVVELLERGAPLLARTKNGLSPLHMAAQGDHVECVKHLLOHKAPVDDVTLDYLTALH 370	
QY	142	SCANC	-----AENEEGCTPLHLACRKGDEILVELVQY-----174
Db	371	VAHCHGYRVTKLLDKRANPNARALNGFTPLHIACKKRIKVMELLVKYGASIQAITES 430	
QY	175	-----CH	-----TQMDVTYKGETVFHYAVQGDNSQVLOLLGRNAVAG 212
Db	431	GLTPHVAAPMGHLNIVLLLLQNGASPDVTNIRGETALHMAARAGQVEVVRCLLRNG-AL 489	
QY	213	LNQVNNQGLTPLHLACQLKQEMVRVLLCNARCINIMPNGY-PIHSAMKFSQKCAEMI 271	
Db	490	VDARAREQTPLHIASRLGKTEIVQLLOHMAHPDAATTNGYTPLHISAREGQVDVASVL 549	
QY	272	ISWDSQIHKSDPRYCASPILHWAK---NAEMAPMLKRCGNVNSTSSAGNTALHVGVMRN 328	
Db	550	--LEAGAAHSLATKKGFTPLHVAARYGSLDVAKLLQRRRAADSAGKGLTPLHVAHYD 607	
QY	329	RFDCAIVLLTHGANADARGEHNTPLHLAMSNDNEMIKALIVFGAEVDTPNDFGETPTF 388	
Db	608	NQKVALLLEKASPHATKNGYTPUHIAAKNQMOIASTLLNYGAETNIVTKQGVTPPLH 667	
QY	389	LASKIG 394	
Db	668	LASQEG 673	

Search completed: May 26, 2005, 14:19:27
Job time : 69.0417 secs

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Db 469 VBARREQTPLHIAIRLUGKTIIVOLLQOHMAHPAAATNGTTPHLHSAREQGVDAVSL 528
Qy 272 ISMSQSIHQDPRYGASPLHWAK---NAEMARMLLKRCNVNNTSSAGNTALHVGVMRN 328
Db 529 --LEAGAHLATKKGFTPLHVAAYGSLDVAKLILQRAADSAGKNGLTPLHVAHYD 586
Qy 329 RFDCAIVLTHGANADAGEHGTPLHLAMSNDVEMIKALIVFGAEVDTPNDFTPTTF 388
Db 587 NOKVALLLEKASPHATAKNGTTPHLHAAKKNQMQIASTLLNYGAETNIVTKQGVTPHL 646
Qy 389 LASKIG 394
Db 647 LASQSG 652

RESULT 15
ANK2 HUMAN
ID ANK2 HUMAN STANDARD; PRT; 3924 AA.
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN Name=ANK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053; DOI=10.1083/jcb.114.2.241;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain ankyrins
RL reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [2]
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844; DOI=10.1083/jcb.123.6.1463;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kD ankyrinB: structure of the major developmentally regulated
RL domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN [4]
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=92009921; PubMed=1833308;
RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RL ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC Name=2;
CC Name=3;
CC Name=4;
CC Name=5;
CC Name=6;
CC Name=7;
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CC Name=1
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RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Iehli Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakeguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Tanahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK044634; BAC32012.1; --
 DR HSSP; P16157; 1N11
 DR MGD; MG1:89025; Ank2.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; Ank; 23.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 23.
 DR PROSITE; PS00888; ANK_REPEAT; 20.
 DR PROSITE; PS0297; ANK_REPEAT; 20.
 DR ANK repeat.
 KW ANK repeat.
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 SQ SEQUENCE 1219 1219 AFB462967AD6184 CRC64;
 Query Match 16.2%; Score 338; DB 2; Length 1219;
 Best Local Similarity 27.6%; Pred. No. 1e-18;
 Matches 101; Conservative 62; Mismatches 126; Indels 77; Gaps 9;
 QY 103 HTEVLQHLTD-----LIRNHPSPVAHLAVELGIRECFHH-----SR11 141
 DB 307 HQQVVELLERKAPLLARTKNGLSPLHMAAQGDHVECVKHLQYKAPVDVTLTYLTALH 366
 QY 142 SCANC-----AENEECTPLHLACRKGDETLVELVQY----- 174
 DB 367 VAAHCHYRVTKLLDKRANPNARALNGFTPLHIAKKNRIKVMELLYKYGASIQAITES 426
 QY 175 -----CH-----TQMDVTDYKGETVFHYAVQGDNSQVLLGRNAVAG 212
 DB 427 GLTPIHVAAFMGHNLIVLLLLQNGASPDVTNIRGETALHMAARAGQVEVVRCLLRNG-AL 485

QY 213 LMQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINIMGPNGY-PIHSAMKFSQKGAEMI 271
 DB 486 VVARAREEQTPHIAIRLKGTEIVQLLQHMADPAATNGYTPPLHISAREGGQVDVASVL 545
 QY 272 ISMDSQIHSKDPYRGASPLHWAK---NAEMARMMLKRCNCNVNSTSSAGNTALHVGVMRN 328
 DB 546 --LEAGAAHSLATKKGFTPLHVAAKYGLSDVAKLLQRRAAADSGKNGLTPLHVAHYD 603
 QY 329 RFDCAVLVLTGHANADARGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTF 388
 DB 604 NQKVALLLERKASPHATAKNGYTPPLHIAAKKNQMOIASTLLNLYGAETNTVTQGVTPHL 663
 QY 389 LASKIG 394
 DB 664 LASQEG 669
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 ID Q7Z3L5 PRELIMINARY; PRT; 1863 AA.
 AC Q7Z3L5; 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFP666H0688.
 GN Name=DKFP666H0688;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human retina;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537758; CAD97827.1; --
 DR HSSP; P55271; 1D9S.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00023; Ank; 23.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00248; ANK; 23.
 DR SMART; SM00005; DEATH; 1.
 DR PROSITE; PS00888; ANK_REPEAT; 20.
 DR PROSITE; PS0297; ANK_REPEAT; 20.
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 SQ SEQUENCE 1863 AA; 204736 MW; 1F4C998E0FOA03DF CRC64;
 Query Match 15.9%; Score 332; DB 2; Length 1863;
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 DB 290 HQQVVELLERKAPLLARTKNGLSPLHMAAQGDHVECVKHLQYKAPVDVTLTYLTALH 349
 QY 142 SCANC-----AENEECTPLHLACRKGDETLVELVQY----- 174
 DB 350 VAAHCHYRVTKLLDKRANPNARALNGFTPLHIAKKNRIKVMELLYKYGASIQAITES 409
 QY 175 -----CH-----TQMDVTDYKGETVFHYAVQGDNSQVLLGRNAVAG 212
 DB 410 GLTPIHVAAFMGHNLIVLLLLQNGASPDVTNIRGETALHMAARAGQVEVVRCLLRNG-AL 468
 QY 213 LMQVNNQGLTPLHLACQLGKQEMVRVLLLCNARCINIMGPNGY-PIHSAMKFSQKGAEMI 271


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DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR002641; Patatin.
DR      Pfam; PF00023; Ank; 4.
DR      PRINTS; PR01734; Patatin; 1.
DR      SMART; SM00248; ANK; 6.
DR      PROSITE; PS50088; ANK_REPEAT; 3.
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KW      ANK repeat.
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Query Match      23.7%; Score 494.5; DB 2; Length 877;
Best Local Similarity 29.2%; Pred.No. 8.5e-32;
Matches 108; Conservative 81; Mismatches 154; Indels 27; Gaps 5;

QY 17 LFSNPRFVAVADYSSDRVREEGQLILFQNTNRTWDCVLNPNRNSQSGFRLPQLEL 76
Db 40 LFAPPF-----NSSNEKAVVEIILQRTSD-----SNTTSPSLYRSPV 78
QY 77 EADALVNFHYQSQQLPFYESSQVLTVEVQLHTLIRNHPNSVAHLAVELGIRECFH 136
Db 79 QOEAEERFNAFLQRLPFVFSIVKEYYVNVGLQKACDALADNPSTLHLIAYPNLVDYIS 138
QY 137 HRIISCANCAENEECTPLHLACRGDGEILLVELVQYCHTQMDVTDYKGETVFHYAVQG 196
Db 139 NPKMLQCVQDAATLMSPPQLAKGHEMVMKALLPL--SKLEHLIDINSNVFHYAA-S 195
QY 197 DNSQVQLLGRNAVAGLNVNNGLTPLHLACQLGQEMVRYVLLNCVRCNTMGPGYPI 256
Db 196 TTKEIINLIIDKSTVNLHNSDGYTPPLHVACLADKPNVKALLAGANVL---NAKDI 252
QY 257 HSAMKFSQKCAEMIIISMDSSQTHSKDPRYGASPLHWAKNAEMARMLKRGCVNNTSSA 316
Db 253 RKVYKTSAPTSSFLRTNVSPLYTQDMKYGGTGPLHWCSSRETLHALIMEGCDVNATFD 312
QY 317 GNTALHVGVMRNEFDCAIVLLTHGANADARGEHNTPLHLANSKNVEMIKALIVPGA 376
Db 313 GRTALHVMVARNRFEVCVWTLAHDABEIDVLVDKDGNAALHIAIEKLVPIVQCLWFGCDI 372
QY 377 DTPNDFGETP 386
Db 373 NLKNGDKGTP 382

RESULT 11
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CG6718-PB (CG6718-pc).
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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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OC Ephydroidea; Drosophilidae; Drosophila.
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008968; BAA13225.1; -.
DR HSSP; P20749; 1K1B.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000560; HisAc_phosphatase.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW ANK repeat.
FT NON TER 1
FT NON TER 879
FT NON TER 879
SQ SEQUENCE 879 AA; 3491E003CF637188 CRC64;

Query Match 24.6%; Score 512; DB 2; Length 879;
Best Local Similarity 29.8%; Pred. No. 3.1e-33;
Matches 113; Conservative 81; Mismatches 175; Indels 10; Gaps 5;

QY 21 PRVKEVAVADYTSDDRVREBQQLILFQNTPNR-----TWDCVLVNPNS--QSGFRLPQ 73
DB 11 PNKQVEVKNESVINLFLVQRNESMRLFAPNPNSPKKLVEILRPHSETINTSYSLYR 70
QY 74 LLEADALVNFQYSSQLLPFFESSPOVLHTEVLHLDLIRNHPSSWSVAHLAVELGTR 133
DB 71 ATTQSAEKEKFAFHORLPVLPVLYREMNYINGLQKCDVLIDNPSWSLAHVAFNLTD 130
QY 134 CFHHSRIISCAENAEECTPLHLACRGDGEILVELVQYCHTQMDVTDYKGTVFHYA 193
DB 131 YISNPSIIDFLDYAEYSMTPLQVAVKANNIEFVKALIQSCNLEHLDKNSVFEHYA 190
QY 194 VQDINSQVQLLGRNAVAGLNQVNOGLTPLHLACQLGQEMVRVLLLCNARCINMGPG 253
DB 191 A-STTKEMINMLTAKSTSLNHCNTDGYTPLHLACLADPCVKALLAGADTNKVA-RG 248
QY 254 YPIHSAMKFSQKGCAMISDSSQTHSKDPRYGASPLHWAKNAEMRLKRGCVNST 313
DB 249 AGTSYSKSTPSSNVADFVLS-NPNKLFQDMKHGGTPLHWSSREVLNLSIEGGCVNLV 307
QY 314 SSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKONVEMKALIVRG 373
DB 308 NFNGQTPLHVMVARDLECVALLAHDAIDVDVNSGNTPLHIAVEKKLPIVQCLVWFG 367
QY 374 AEVDTPNDPGETPTFLASK 392
DB 368 ADFNPNKDGKTPRHLVGK 386

RESULT 10
ID Q9VT60 PRELIMINARY; PRT; 877 AA.
AC Q9VT60;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG6718-PA.
OS ORFNames=CG6718;
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RL melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RL a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
```

SQ	SEQUENCE	756 AA; 84303 MW; C0278741CCA52A71 CRC64;
Query Match	56.4%; Score 1176; DB 2; Length 756;	
Best Local Similarity	54.3%; Pred. No. 5.5e-88;	
Matches 213; Conservative	86; Mismatches 93; Indels 0; Gaps 0;	
QY	1 MQPFGRLVNTFSGVTNLFNSNPFVKVAVADYTSDDRVREBEGQILFQNTPNRTWDCVLV 60	
DB	1 MDLFGRIFTVSAVTNLFNSNPFVKVREPLSEYSGSSCLQBDGRLMYRNRATAKSLDCVLV 60	
QY	61 NPNSSQSGRLFOLEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPW 120	
DB	61 NPSPPONAKLFOLESEPEALCFQYAVKRLPFYESSRKGCLCLETLOQLTDCIRSHPNW 120	
QY	121 SVAHLAVELGIRCFHHSRIISCANCAENEBGCTPLHLACRKGDBGILVELVOYCHTQMD 180	
DB	121 SLAHVAVEIGLRSEFKHNGILRLNTECDGGSTPLHLACKGDINCLQELVECEQARLD 180	
QY	181 VTDYKGETVFHYAVQSDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240	
DB	181 IADQNGETVYHAAQQNNPRVIBILCSVPSGVGNHKSNNNETPLHVACRLGKTELVALL 240	
QY	241 LCNARCINMGPNGYPIHSAKMFQKGCACMIISMDSQIHSKDPDPRYGASPLHWAKNAEMA 300	
DB	241 RCHARCDDIIGKQGYPIHTAMKYQKCEVAILDVSASQLHAEDPRYQATPIHWAKNAEMA 300	
QY	301 RMLKRGCVNNTSSAGNTALHVGWNRNPDCAIVLLTHGANADARGEHGTPLHLAMSK 360	
DB	301 RLBIERGCVNNTCKLDTPLHITVWRDRPEAAWLLTNVADPNVGEHGTPLHLAMKK 360	
QY	361 DNVEMIKALIVFGAEDVTNDFGETPTFLASK 392	
DB	361 DQLELIKALMVFGADVEQHNDFGETPLGIAR 392	
RESULT 8		
Q6NWY0		
ID	O6NWY0 PRELIMINARY; .PRT; 818 AA.	
AC	O6NWY0;	
DT	05-JUL-2004 (TREMBlrel. 27, Created)	
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)	
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)	
DE	Zgc:77476.	
GN	ORFNames=zgc:77476;	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Kidney;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.G., Hulyk S.W.,	
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	

RN	SEQUENCE FROM N.A.	
RP	TISSUE=Kidney;	
RA	Strausberg R.;	
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC067375; AAH67375.1; -	
DR	HSSP; P20749; 1K1B.	
DR	ZFIN; ZDB-GENE-040426-2079; zgc:77476.	
DR	GO; GO:0003824; F: catalytic activity; IEA.	
DR	GO; GO:0045735; F: nutrient reservoir activity; IEA.	
DR	InterPro; IPR002110; ANK.	
DR	InterPro; IPR002641; Patatin.	
DR	Pfam; PF00023; Ank; 6.	
DR	PRINTS; PR01734; Patatin; 1.	
DR	SMART; SM00248; ANK; 6.	
DR	PROSITE; PS00088; ANK_REPEAT; 4.	
DR	PROSITE; PS00297; ANK_REPEAT; 1.	
KW	ANK repeat.	
SQ	SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;	
Query Match	49.8%; Score 1037.5; DB 2; Length 818;	
Best Local Similarity	48.7%; Pred. No. 1.5e-76;	
Matches 191; Conservative	87; Mismatches 113; Indels 1; Gaps 1;	
QY	1 MOFFGRLVNTFSGVTNLFNSNPFVKVAVADYTSDDRVREBEGQILFQNTPNRTWDCVLV 60	
DB	1 MQPFGRLITVSVSSLSFNSNPFVRVDVQLSDYNGKILHQEGRLALYRNOQSQSWDCLLL 60	
QY	61 NPNSSQSGRLFOLEADALVNFHQYSSQLLPFYESSQVLHTEVLOHLTDLIRNHPW 120	
DB	61 CPESPSVALRMFQVASEEDAMNWFQYALKRPFYEMLRPLKPEMLQPIVDCVRNHPDW 120	
QY	121 SVAHLAVELGIRCFHHSRIISCANCAENEBGCTPLHLACRKGDBGILVELVOYCHTQMD 180	
DB	121 SSAHIAVDTGLRDLCKLHNYILSQMN-SRDAQGQTPHLACERGDVGVRELLSECOARTD 179	
QY	181 VTDYKGETVFHYAVQSDNSQVLQLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240	
DB	180 VDKNGETPMHCAAKQDSALIEVLCAQLCAGVNNELNAAGETPMHIACTGRVVEVVGKLL 239	
QY	241 LCNARCINMGPNGYPIHSAKMFQKGCACMIISMDSQIHSKDPDPRYGASPLHWAKNAEMA 300	
DB	240 AGGARCDIMGNGGFPPIHTAMKSEKSCAEALISSPNQLLAEDPVYGGTPLHWAKTAEWS 299	
QY	301 RMLKRGCVNNTSSAGNTALHVGWNRNPDCAIVLLTHGANADARGEHGTPLHLAMSK 360	
DB	300 RLLDRGCVNNTSKTGESPLHILTKRGFEAAWLLTHGADANIRGQDNTALHLAMKL 359	
QY	361 DNVEMIKALIVFGAEDVTNDFGETPTFLASK 392	
DB	360 DNMDLIKALMVFGADVEHNDVGETPLGIAR 391	
RESULT 9		
Q7Q2U1		
ID	Q7Q2U1 PRELIMINARY; .PRT; 879 AA.	
AC	Q7Q2U1;	
DT	01-MAR-2004 (TREMBlrel. 26, Created)	
DT	01-MAR-2004 (TREMBlrel. 26, Last sequence update)	
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)	
DE	EbiP3359 (Fragment).	
GN	Name=ebg3359; ORFNames=ENSGG000000002698;	
OS	Anopheles gambiae str. PEST.	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.	
OX	NCBI_TaxID=180454;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=PEST;	
RA	Anopheles Genome Sequencing Consortium;	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
CC	!- CAUTION: The sequence shown here is derived from an	

RP SEQUENCE FROM N.A.
 RC STRAIN:Sprague-Dawley; TISSUE=Pancreatic islets;
 RX MEDLINE=97269008; PubMed=9111008; DOI=10.1074/jbc.272.17.11250;
 RA Ma Z., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.;
 RT "Pancreatic islets express a Ca²⁺-independent phospholipase A2 enzyme
 RT that contains a repeated structural homologous to the integral
 RT membrane protein binding domain of ankyrin.",
 RL J. Biol. Chem. 272:11118-11127(1997).
 CC -!- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and
 CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
 CC heart and skeletal muscle.
 CC -!- SIMILARITY: Contains 7 ANK repeats.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U51898; AAC53136.1; -;
 DR HSP; Q60778; I0Y3.
 DR GSD; 628867; Fla296.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ANK; 6.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
 FT REPEAT 150 180 ANK 1.
 FT REPEAT 184 214 ANK 2.
 FT REPEAT 218 247 ANK 3.
 FT REPEAT 250 280 ANK 4.
 FT REPEAT 285 311 ANK 5.
 FT REPEAT 315 344 ANK 6.
 FT REPEAT 348 377 ANK 7.
 FT ACT SITE 464 464 Potential.
 SQ SEQUENCE 751 AA; 83582 MW; 393BBBADA7FCC99B CRC64;
 Query Match 86.8%; Score 1808.5; DB 1; Length 751;
 Best Local Similarity 86.8%; Pred. No. 4.6e-140;
 Matches 341; Conservative 20; Mismatches 31; Indels 1; Gaps 1;
 QY 1 MPPFGLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
 DB 1 MPPFGLVNTFSGVTLNFSNPRVKEVAVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
 QY 61 NPNRSQSGFRLQLEADALVNFHOYSSQLLPFYESSPQVLHTEVLQHLTLIRNHPWS 120
 DB 61 SPNPNQSDRLQLESEADVLNVFQYSSQLPPFYESSQVLHVEVLQ-LTDLIRNHPWS 119
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENBEGCTPLHLACRKGDSILVELVQYCHTQMD 180
 DB 120 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVQYCHAQMD 179
 QY 181 VTDYKGETVHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
 DB 180 VTDNKGETAHYAVQGDNPQVLQLLGNKNAVAGLNQVNNQGLTPLHLACQMGQEMVRVLL 239
 QY 241 LCNARCINMGPNGYPTHSAKTSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAENA 300
 DB 240 LCNARCINMGPGFPIHTANKFSQKCAEMIIISMDSNQIHSKDPYRGASPLHWAKNAENA 299

QY 301 RMLLRGCGNVNSTSAGNTALHVGVMRNFDCAIUVLLTHGANADARGHGNTPLHLAMSK 360
 DB 300 RMLLRGCGVDSTSGNTALHVAVTRNFDVWVLLTYGANAGARGHGNTPLHLAMSK 359
 QY 361 DNVEIKALIVFGAEVDTPNDFGETPTFLASKI 393
 DB 360 DNMEVAKALIVFGAEVDTPNDFGETPTAFIASKI 392
 RESULT 7
 Q6DDKO PRELIMINARY; PRT; 756 AA.
 AC Q6DDKO;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DE MGC83523 protein.
 GN Name=MGC83523;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=223441132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC077558; AAH77558.1; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF00023; Ank; 7.
 DR Pfam; PF01734; Patatin; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 7.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.

Db	121	TVTHLAVELGTRCFHSHRIISCANSTENEGCTPLHLACRCKGDSILVELVOYCHAQMD	181
Qy	181	VTDYKGETVFHYAVQGDNSQVQLLGLGRNAVAGLNQVNNQGLTFLHLACQLGQKQEMVRVLL	240
Db	181	VTDNKGETAFHYAVQGDNPQVQLLGLGNASAGLNQVNNQGLTFLHLACRCKGQKQEMVRVLL	240
Qy	241	LCNARCNTMGPNQYPIHSAMKFSQKGCACMIISMDSSQIHSKDPYRGASPLHWAKNAEWA	300
Db	241	LCNARCNTMGPGGPIIHTAMKFSQKGCACMIISMDSNQIHSKDPYRGASPLHWAKNAEWA	300
Qy	301	RMLLKRGCGNVNSTSSAGNTALHVGVMNRNRFDCIAVLTLTHGCANADARGEHGNTPLHLAMSK	360
Db	301	RMLLKRGCGVDVSTSSGNTALHVAVMNRNRFDCVNVLLTYGANNAGARGEHGNTPLHLAMSK	360
Qy	361	DNVEMIKALIVFGAEVDTPNDPFGETPTFFLASKI	393
Db	361	DNMVMKALIVFGAEVDTPNDPFGETPTALIASKI	393
RESULT 4			
Q9JUK61			
ID	Q9JUK61	PRTEINIMINARY;	PRT; 807 AA.
AC	Q9JUK61;		
DT	01-OCT-2000	(TREMBLrel. 15, Created)	
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)	
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)	
DE	Ca2+-independent phospholipase A2 long form (Pla2g6 protein).		
DE	Name=Pla2g6;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=NIH/Swiss;		
RC	Chiu C.-H., Jackowski S.;		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RN	STRAIN=NMRI; TISSUE=Mammary tumor;		
RN	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[3]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=NMRI; TISSUE=Mammary tumor;		
RA	Strausberg R.;		
RL	Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF259401; AAF72651.1; -		
DR	EMBL; BC057209; AAH57209.1; -		
DR	HSSP; O60778; 10Y3		
DR	MGD; MGI:1859152; Pla2g6.		
DR	GO; GO:0003824; F:catalytic activity; IEA.		
DR	GO; GO:0045735; F:nutrient reservoir activity; IEA.		
DR	InterPro; IPR002110; ANK.		

DR HSP; Q60778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 99.7%; Score 2078; DB 1; Length 806;
Best Local Similarity 99.7%; Pred. No. 3.3e-162;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTFSGVNTLFSNPRFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTFSGVNTLFSNPRFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60

QY 61 NPNRSQSGFRLQLLEADALVNFHQYSSQLLPFFYESSQVLHTEVQLHQLTDLIRNHPWS 120
Db 61 NPNRSQSGFRLQLLEADALVNFHQYSSQLLPFFYESSQVLHTEVQLHQLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 SVAHLAVALGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLVNNOGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLVNNOGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLKRGCVNSTSSAGNTALHGVNRRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLKRGCVNSTSSAGNTALHGVNRRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTNDGFTPLFLASKIG 394
Db 361 DNVEIMKALIVFGAEVDTNDGFTPLFLASKIG 394

RESULT 2
ID Q66HD1 PRELIMINARY; PRT; 807 AA.
AC Q66HD1;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC081916; AAH81916.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patatin.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK REPEAT; 4.
DR PROSITE; PS50297; ANK REP REGION; 1.
KW ANK repeat, Hypothetical protein.
SQ SEQUENCE 807 AA; 89555 MW; 1B9018AE1B2D252F CRC64;

Query Match 88.8%; Score 1851; DB 2; Length 807;
Best Local Similarity 88.3%; Pred. No. 1.6e-143;
Matches 347; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 1 MQFFGRLVNTFSGVNTLFSNPRFRVKEVAVADYTSSDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MQFFGRLVNTLSSVNTLFSNPRFRVKEVSLADYASSRVEREGLIILQNASNRTWDCVLV 60

QY 61 NPNRSQSGFRLQLLEADALVNFHQYSSQLLPFFYESSQVLHTEVQLHQLTDLIRNHPWS 120
Db 61 SPRNPQSGFRLQLLEADALVNFQYSSQLPPFFYESSQVLHTEVQLHQLTDLIRNHPWS 120

QY 121 SVAHLAVALGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 TVTHLAVALGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHQAMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLQGRNAVAGLVNNOGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNGETAFHYAVQGDNPQVLQGLGNASAGLVNNOGLTPLHLACOLGKQEMVRVLL 240

QY 241 LCNARCINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCINMGPGFPIHTAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLKRGCVNSTSSAGNTALHGVNRRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLKRGCDVDSTASGNTALHVAVTRNRFDCVVMVLLTYCANAGARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDTNDGFTPLFLASKI 393
Db 361 DNMEWVKALIVFGAEVDTNDGFTPAFIASKI 393

RESULT 3
PA26 MOUSE
ID PA26 MOUSE STANDARD; PRT; 752 AA.
AC P97819; Q99LA9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-
FLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX BALBOA M.A., Balsinde J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
P38D1 macrophages and Chinese hamster ovary cells.";
RL J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:06:44 ; Search time 64.0417 Seconds
(without alignments)
3150.433 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MQFFRLVNTFSGVNLFNSN.....EVDTPNDFGTPTFLASKIG 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2078	99.7	806	1 PA26 HUMAN	O60733 homo sapien
2	1851	88.8	807	2 Q66HD1	Q66hd1 rattus norv
3	1842	88.4	752	1 PA26 MOUSE	P97819 mus musculu
4	1842	88.4	807	2 Q9JKE1	Q9jke1 mus musculu
5	1832	87.9	752	2 Q7TFX2	Q7tfx2 mus musculu
6	1808.5	86.8	751	1 PA26 RAT	P97570 rattus norv
7	1176	56.4	756	2 Q6DDK0	Q6ddk0 xenopus lae
8	1037.5	49.8	818	2 Q6NWO0	Q6nwo0 brachydanio
9	512	24.6	879	2 Q7Q2U1	Q7q2u1 anopheles g
10	494.5	23.7	877	2 Q9VT60	Q9vt60 drosophila
11	494.5	23.7	887	2 Q7KUD4	Q7kud4 drosophila
12	338	16.2	843	2 P97582	P97582 rattus norv
13	338	16.2	1219	2 Q8C8R3	Q8c8r3 mus musculu
14	332	15.9	1863	2 Q723L5	Q723l5 homo sapien
15	332	15.9	3924	1 ANK2 HUMAN	Q01484 homo sapien
16	318	15.3	1004	2 Q7JNZ0	Q7jnz0 caenorhabdi
17	318	15.3	1786	2 Q17344	Q17344 caenorhabdi
18	318	15.3	1809	2 Q17487	Q17487 caenorhabdi
19	318	15.3	1815	2 Q17488	Q17488 caenorhabdi
20	318	15.3	1841	2 Q8MGO3	Q8mgo3 caenorhabdi
21	318	15.3	1867	2 Q17486	Q17486 caenorhabdi
22	318	15.3	2039	2 Q17489	Q17489 caenorhabdi
23	318	15.3	6994	2 Q17343	Q17343 caenorhabdi
24	318	15.3	6994	2 Q17490	Q17490 caenorhabdi
25	313.5	15.0	1549	2 Q24241	Q24241 drosophila
26	313.5	15.0	1549	2 Q9V4B1	Q9v4b1 drosophila
27	310	14.9	1009	2 Q8SWY2	Q8swy2 drosophila
28	310	14.9	1159	2 Q9NCP8	Q9ncp8 drosophila
29	310	14.9	1571	2 Q7KUR2	Q7ku92 drosophila
30	305.5	14.7	792	2 Q7Q172	Q7q172 anopheles g
31	304.5	14.6	820	2 Q8JHU3	Q8jhu3 brachydanio

32	301	14.4	786	2 Q9ERK0	Q9erk0 mus musculu
33	298	14.3	2622	2 Q70511	Q70511 rattus norv
34	296	14.2	1088	2 Q13484	Q13484 homo sapien
35	296	14.2	4377	1 ANK3 HUMAN	Q12955 homo sapien
36	295.5	14.2	1145	2 Q7FEZ8	Q7pez8 anopheles g
37	295.5	14.2	1501	2 Q7QKD3	Q7qkd3 anopheles g
38	295.5	14.2	1887	2 Q723G4	Q723g4 homo sapien
39	294.5	14.1	1136	2 Q9N180	Q9n180 bos taurus
40	294	14.1	1719	2 Q13768	Q13768 homo sapien
41	294	14.1	1856	2 Q99407	Q99407 homo sapien
42	294	14.1	1880	1 ANK1 HUMAN	P16157 homo sapien
43	293	14.1	1726	2 Q8VC68	Q8vc68 mus musculu
44	293	14.1	1943	2 Q61307	Q61307 mus musculu
45	290.5	13.9	1614	2 Q7TIG6	Q7tig6 brachydanio

ALIGNMENTS

RESULT 1

PA26 HUMAN STANDARD; PRT; 806 AA.
AC O60733; Q75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6; Synonyms=IPLA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2).
RC TISSUE=B-cell, and Testis;
RX MEDLINE=98079046; PubMed=9417066; DOI=10.1074/jbc.273.1.207;
RA Larsson P.K.A., Claesson H.-E., Kennedy B.P.;
RT "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity.";
RL J. Biol. Chem. 273:207-214 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2).
RC TISSUE=Pancreatic islets;
RX MEDLINE=99194813; PubMed=10092847; DOI=10.1074/jbc.274.14.9607;
RA Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.;
RT "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1.";
RL J. Biol. Chem. 274:9607-9616 (1999).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99269033; PubMed=10336645;
RA Larsson Forsell P.K.A., Kennedy B.P., Claesson H.-E.;
RT "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene.";
RL Eur. J. Biochem. 262:575-585 (1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM LH-IPLA).
RC TISSUE=Testis;
RA Ansonge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schnackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1862 <RES>

A:Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940

C:Genetics:

A:Gene: Ank-1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:40-72/Domain: ankyrin repeat homology <AN01>

F:73-105/Domain: ankyrin repeat homology <AN02>

F:106-138/Domain: ankyrin repeat homology <AN03>

F:139-167/Domain: ankyrin repeat homology <AN04>

F:168-200/Domain: ankyrin repeat homology <AN05>

F:201-233/Domain: ankyrin repeat homology <AN06>

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F:267-299/Domain: ankyrin repeat homology <AN08>

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F:498-530/Domain: ankyrin repeat homology <AN15>

F:531-563/Domain: ankyrin repeat homology <AN16>

F:564-596/Domain: ankyrin repeat homology <AN17>

F:597-629/Domain: ankyrin repeat homology <AN18>

F:630-662/Domain: ankyrin repeat homology <AN19>

F:663-695/Domain: ankyrin repeat homology <AN20>

F:696-728/Domain: ankyrin repeat homology <AN21>

F:729-761/Domain: ankyrin repeat homology <AN22>

F:762-794/Domain: ankyrin repeat homology <AN23>

Query Match 13.7%; Score 285; DB 2; Length 1862;

Best Local Similarity 25.6%; Pred. No. 1.7e-15;

Matches 93; Conservative 55; Mismatches 121; Indels 94; Gaps 10;

QY 107 LOHLDLIRNHFSSVAHLAVELGIRECPHH--SRIISCANCAENE---EGCTPLHLACR 161

DB 332 LDHLTPL-----HVAA-----HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIACK 376

QY 162 KGDGEILVELVQYCHTQMD-----VTDYKGET 188

DB 377 KKHIRMV-ELLKKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKET 435

QY 189 VEHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQIGKQEMVRVLLCNARCN 248

DB 436 PLHMAARAGHTEVAKYLLQNK-AKANAKAKDQDTPLHCAARIGTGTGMVKLLLENGASPNL 494

QY 249 MGPNGY-----PIHSAMKFSQKGCAMIISM 274

DB 495 ATTAGHTPLHTAAREGHVDTALALLEKEASQACMTKKGFTPLHVAAKYGVRLAELLLEH 554

QY 275 DSSQIHSKDPYRGASPLHWA---KNAEMARMLKRCNVNSTSSAGNTALHVGVMNRNF 331

DB 555 DAHP--NAAGKNGTLPVAVHNNLDIVKLLPRGSGSPHSPAWNGYTPPLHIAAKNQIE 612

QY 332 CAIVLTHGANADARGEHNTPLHLSKDNVEMIKALIVFGAEVDTPNDFGETPTFLAS 391

DB 613 VARSLLQYGGSSANAESVQGVTPPLHAAQBGHTEWVALLLSKQANGNLGNKSLGTLPLHLVS 672

QY 392 KIG 394

DB 673 QEG 675

RESULT 15

T46445

hypothetical protein DKFp434B2328.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46445

R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23032

A:Accession: T46445

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-397 <AAA>

A:Cross-references: UNIPROT:Q9NTAL; EMBL:AL137448

A:Experimental source: adult testis; clone DKFZp434B2328

C:Genetics:

A>Note: DKFZp434B2328.1

Query Match 13.5%; Score 281.5; DB 2; Length 397;

Best Local Similarity 30.7%; Pred. No. 4.2e-16;

Matches 86; Conservative 48; Mismatches 135; Indels 11; Gaps 7;

QY 121 SVAHLAVELGIRECPHHRIISCANCAENEECTPLHLAC-RKGDGEILVELVQYCHTOM 179

DB 53 SILHLAVEAGQECACAKWLLNANPNLSNRRGSTPLHMAVERVRG--VVLELLARKISV 110

QY 180 DVTDYKGETVEHYAVQ-GDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQIGKQEMVRV 238

DB 111 NAKDEQWLTALHFAAQNGDESSTRLLLEKN--ASVNEVDTEGRTPMHVACQHGQENIVRI 168

QY 239 LLLCNARCINMGPGY-PIHSAMKFSQKGCAMIISMDSQIHSKDPYRGASPLHWAK-- 295

DB 169 LLRRGVTVSLQGDWLPVHYAAWQCHLPVVKLLAKQPGVSNQAQ-TLDGRTPLHLAQR 227

QY 296 -NAEMARMLKRCNVNSTSSAGNTALHVGVMNRNPDCAIVLLTHGANADARGEHNTPL 354

DB 228 GHYRVARILIDLCSQVNVVCSLLAQTPHVAARETGTSTARLLHLHRGAGKEAVTSDGYTAL 287

QY 355 HLAMSKDNVEMIKALIVFGAEVDTENDFGETPTFLASKIG 394

DB 288 HLAARNGHLATVKLLIVEEKADVLARGPLNQTLALHAAAAG 327

Search completed: May 26, 2005, 14:20:31

Job time : 14.279 secs

F:597-629/Domain: ankyrin repeat homology <AN17>
 F:630-662/Domain: ankyrin repeat homology <AN18>
 F:663-695/Domain: ankyrin repeat homology <AN19>
 F:696-728/Domain: ankyrin repeat homology <AN20>
 F:729-761/Domain: ankyrin repeat homology <AN21>
 F:762-794/Domain: ankyrin repeat homology <AN22>
 F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 14.2%; Score 296; DB 2; Length 4377;
 Best Local Similarity 29.2%; Pred. No. 6.5e-16;
 Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;

QY 124 HLAVELGIRECFHRSRIISCANCAENESECTPLHLACRKGDEILVELVOYCHTOMDVTD 183
 DB 504 HISARLGRADIVQQLQOQASNAATTSGYTPHLHSAREGHEDVAFLLDH-GASLSITT 562
 QY 184 YKGETVFHVAVQGDNSQVLQLGRNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLLCN 243
 DB 563 KGFTPLHVAKYGKLEVANLLQKS-ASPDAGKSGLTPLHVAHYDNQKVALLLDQ 621
 QY 244 ARCNTMGNGY-PIHSAMKFSQKGAEMII--SMDSSQIHSKDPYRGASPLHWAK---NA 297
 DB 622 ASPHAAKNGYTPHLHAAKKNQMDIATTLLEYGADANAV---TRQGIASVHLAAQEGHV 677
 QY 298 ENARMLLKRCGNVNTSSAGNTALHVGWVRNRFDCAIVLLTHGANADARGEHGTPLHLA 357
 DB 678 DMVSLLRGNANVNLNKSGLTPLHLAAQEDRVNVAEVLVNGAHVDAQTRMGYTPLVHG 737
 QY 358 NSKDNVEMKALIVGAEDVTENDFGETPTFLASKIG 394
 DB 738 CHYGNIKIWNFLQHSKAKVNAKNGYTPHLHQAQOQ 774

RESULT 6

B35049
 ankyrin 1, erythrocyte splice form 3 - human
 N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contains: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 C:Accession: B35049
 R:Lambert, S.; Yu, H.; Prochal, J.T.; Lawler, J.; Ruff, P.; Speicher, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A:Title: cDNA sequence for human erythrocyte ankyrin.
 A:Reference number: A35049; MUID:90175370; PMID:1689849
 A:Accession: B35049
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1856 <LAM>
 C:Genetics:

A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 A:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing
 F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
 F:2-1513.1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
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 F:77-109/Domain: ankyrin repeat homology <AN02>
 F:110-142/Domain: ankyrin repeat homology <AN03>
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 F:205-237/Domain: ankyrin repeat homology <AN06>
 F:238-270/Domain: ankyrin repeat homology <AN07>
 F:271-303/Domain: ankyrin repeat homology <AN08>
 F:304-336/Domain: ankyrin repeat homology <AN09>
 F:337-369/Domain: ankyrin repeat homology <AN10>
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 F:403-435/Domain: ankyrin repeat homology <AN12>
 F:436-468/Domain: ankyrin repeat homology <AN13>
 F:469-501/Domain: ankyrin repeat homology <AN14>
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 F:601-633/Domain: ankyrin repeat homology <AN18>
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 F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 14.1%; Score 294; DB 2; Length 1856;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLRNPSVSAHLAVELGIRECFH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLTPL-----HVAA-----HGHHRVAKVLLDKGAKPNSRALNGFTPLHIACK 380
 QY 162 KGDGEILVELVOYCHTOMD-----PIHSAMKFSQKGAEMIIISM 274
 DB 381 KHVVRVM-ELLKTKASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNVKVET 439
 QY 189 VFHVAVQGDNSQVLQLGRNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLLCNARCN 248
 DB 440 PLHMAARAGHTEVAKYLLQNK-AKYNAKAKDDQTPHCAARIGHTNMVKLLLENNANPNL 498
 QY 249 MGPNGY-----PIHSAMKFSQKGAEMIIISM 274
 DB 499 ATTAGTTPHIAAREGHVETVLAALLEKEASQACMTKGFTPLHVAKYGKVRVAELLER 558
 QY 275 DSSQIHSKDPYRGASPLHWA---KNAEMARMLLKRCGNVNTSSAGNTALHVGWVRNRF 331
 DB 559 DAHP--NAAKNGLTPLHVAHVHNNLDIVKLLPRGSGPHSPAWNNGYTPHLHAAKQNOVE 616
 QY 332 CAIVLLTHGANADARGEHGTPLHLAMSKDNVEMKALIVFGAEVDTNDPFGETPTFLAS 391
 DB 617 VARSLLQYGGSSANAESVQGVTPHLAAQEGHAEVALLSKQANGNLGKSLTPLHLVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 7

B35049
 ankyrin 1, erythrocyte splice form 2 - human
 N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N:Contains: ankyrin 2.2, erythrocyte
 C:Species: Homo sapiens (man)
 C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004
 C:Accession: A35049
 R:Lambert, S.; Yu, H.; Prochal, J.T.; Lawler, J.; Ruff, P.; Speicher, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A:Title: cDNA sequence for human erythrocyte ankyrin.
 A:Reference number: A35049; MUID:90175370; PMID:1689849
 A:Accession: A35049
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1880 <LAM>
 A:Cross-references: UNIPROT:P16157; GB:M28880
 C:Genetics:

A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 A:Superfamily: ankyrin; ankyrin repeat homology
 C:Keywords: alternative splicing; cytoskeleton
 F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F:2-1513.1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F:44-76/Domain: ankyrin repeat homology <AN01>
 F:77-109/Domain: ankyrin repeat homology <AN02>
 F:110-142/Domain: ankyrin repeat homology <AN03>
 F:143-171/Domain: ankyrin repeat homology <AN04>
 F:172-204/Domain: ankyrin repeat homology <AN05>
 F:205-237/Domain: ankyrin repeat homology <AN06>
 F:238-270/Domain: ankyrin repeat homology <AN07>

A>Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *C. elegans*
A:Reference number: A57282; MUID:95263663; PMID:7744957
A:Accession: A57282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-852; GGG, 856-1000, 'SKLQHT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'B', 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS', <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: B57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'B', 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS', <OTS>
A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
A:Accession: C57282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, '4', 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVTT', 1944, 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVTT', 1944
A:Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
C:Genetics:
A:Gene: CESP.unc-44
A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979/2
C:Superfamily: ankyrin; ankyrin repeat homology
F:164-192/Domain: ankyrin repeat homology <AN04>
F:358-390/Domain: ankyrin repeat homology <AN1>
F:391-423/Domain: ankyrin repeat homology <AN11>
Query Match 15.3%; Score 318; DB 2; Length 2039;
Best Local Similarity 33.6%; Pred. No. 3.1e-18;
Matches 86; Conservative 49; Mismatches 105; Indels 16; Gaps 6;
QY 147 AENEGCTPLHACRGDGEILVELVOYCHTQMDVTDYKGETVHFVAVOGDINSQVLLQAG 206
DB 420 ATTESGLTPLHVAAFMGAINIYVLLQQ-GANPDVETVRGETPLHAAARANDVVRVLI 478
QY 207 RNAVAGLNQVNNQGLTPLHLAQLGKQEMVRVLLLCNARCINMGPNY-PIHSAMKFSQK 265
DB 479 RNG-AKVDAQARELQTPHLIASRLGNVDIVILLQAGANSNATRDYNSPLHIAKEGQE 537
QY 266 GCAEMIISWDSSQIHSKD---PRYGASPLHWAK---NAEMARMLLKRCNVSSTSSAGN 318
DB 538 EVAGILLD-----HNADKTLTKKGFTPLHLASKYGNLEVVRLLEERGTPVDIEGKNQV 591
QY 319 TALHVGWENRFDCAVLVLTGKANADARGEHNTPLHLSKDNVEMIKALIVGAEVDT 378
DB 592 TPLHVAHYNNDKVAMLLLENGASAKAAKNGYTPPLHIAAKKNQMEIATLLQKADPNA 651
QY 379 PNDFGETPTFLASKIG 394
DB 652 KSRAGFTPLHLSAQEG 667
RESULT 4
T13940
Ankyrin - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13940
R:Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A>Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in *Drosophila*
A:Reference number: Z17820; MUID:95024098; PMID:7937942
A:Accession: T13940
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1549 <DUB>
A:Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:g557083; PID:g557084; PIDN:AAC37208
C:Genetics:
A:Cross-references: FlyBase:FBgn0011747
Query Match 15.0%; Score 313.5; DB 2; Length 1549;
Best Local Similarity 23.9%; Pred. No. 5.1e-18;

Matches 114; Conservative 68; Mismatches 144; Indels 151; Gaps 16;
QY 45 ILFQNTPNRTWDCVLVNPNSOSGPRFLFOLELEADALVNFQYSSOLL-----PFYESSP 99
DB 319 LIQQNAP-----ILTKYNGLSALHM-----AAQGEHDEAAHLLDNKAPVDEVTV 364
QY 100 QVL-----HTEVLQHLTDLIRNHP-----WSVAHLA-----VELGIRECFH 136
DB 365 DVLTAHLVAACHGVKAVKLLDYKANPNARALNGFTPLHIAACKNRIKMWELLIK--H 421
QY 137 HSRILISCANENEGCTPLHACRGDGEILVELVOYCHTQMDVTDYKGETVHFVAVOG 196
DB 422 GANI-----GATTESGLTPLHVASFGCINIVYLLQH-EASADLPTIRGETPLHLAAR 475
QY 197 DNSQVQLQLGRNAV-----210
DB 476 NQADIIRILRSKVDIAVREGQTPHVASRLGNINIMLLQHGAEINNAQSNKYSAHL 535
QY 211 -----AGLNQVNNQGLTPLHLAQLGKQEMVRVLLLCNARCINMGPN 252
DB 536 IAAKSGQENIVQVLLLENGAENNAVTKGFTPLHLACKYQNVVQVLLQNGASIDFGKN 595
QY 253 GY-PIHSAMKFSQKCAEMIISWDSS-----QI--HSDK- 283
DB 596 DVTPLHVAHYNNPSIVLELLKNGSSPNLCARNGQCAIHIACKKNYLEIAMQLLQHGADV 655
QY 284 ---PRYGASPLHWAK---NAEMARMLLKRCNVSSTSSAGNTALHVGWENRFDCAVLV 337
DB 656 NIISKSGFSPHLAAQGGNVDMVQLLEYGV-ISAANKGLTPLHVAAGHGVLVLSQILL 714
QY 338 THGANADARGEHNTPLHLSKDNVEMIKALIVGAEVDTNDFGFTPTFLASKIG 394
DB 715 EHGANISERTRNGYTPHVAHYHGLDLYKFFIENDADIEMSSNIGYTPHLQAQOG 771
RESULT 5
A55575
Ankyrin 3, long splice form - human
N:Alternate names: ankyrin G
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C:Accession: A55575
R:Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A>Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax
A:Reference number: A55575; MUID:95138209; PMID:7836469
A:Accession: A55575
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-4377 <KOR>
A:Cross-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
C:Genetics:
A:Gene: GDB:ANK3
A:Cross-references: GDB:424503; OMIM:600465
A:Map position: 10q21-10q21
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C:Keywords: alternative splicing; peripheral membrane protein
F:73-105/Domain: ankyrin repeat homology <AN01>
F:106-138/Domain: ankyrin repeat homology <AN02>
F:139-171/Domain: ankyrin repeat homology <AN03>
F:172-200/Domain: ankyrin repeat homology <AN04>
F:201-233/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>

F;694-726/Domain: ankryrin repeat homology <AN20>
F;727-759/Domain: ankryrin repeat homology <AN21>
F;760-792/Domain: ankryrin repeat homology <AN22>
F;793-825/Domain: ankryrin repeat homology <AN23>

Query Match 15.9%; Score 332; DB 2; Length 3924;
Best Local Similarity 27.3%; Pred.No. 4.8e-19;
Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;

QY 103 HTEVLQHLLTD-----LIRNHPSSVAHLAVELGIRECFHH-----SRII 141
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 311 HDQVVELLLERGAFLARTKNGLSPLHMAAQGDHVCEVKHLLQHKAPDDVTLDLTALH 370
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 142 SCANC-----AENEECTPLHLACRKDGEILVELVOY----- 174
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 371 VAAHCCHYRVTKLLDKRANPNARALNGFTPLHIACKKNRIKVMELLVKYGASIQAITES 430
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 175 -----CH-----TQMVDYKYGETVFHYAVOGDNSVLQLGRNAVAG 212
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 431 GLTPIHVAAFMGHLNIIVLLLLQNGASPDVTNIGRETALHMAARAGQEVVRCLLRNG-AL 489
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 213 LNQVNNOGLTPLHLACOLGKGEMVRVILLNCARNIMGNGY-PHSAMKFSGKCAEMI 271
:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 490 VDARAREOQPLHTASRLCKTEIVOLLQHWHPDAATNGTPTPLHISAREGOVDVASVL 549
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 272 ISMDSQTHSKDPRYGASPLHWAK---NAEMARMELLKRGCNVNSTSSAGNTALHVGVMRN 328
:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 550 --LEAGAASHLATKKGFPTFLHVAAYKGSGLDVAKLLQRRAADSAGKNGLTPLHVAAHYD 607
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 329 RFDCAIIVLLTHGANADARGEIGNTPPLHAMSNDVEMIKALIVFGAEVDTPNDFGETPTTF 388
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 608 NQKVALLLEKGSFHATAKNGYTPLHTAAKNQMQIASTLLNYGAETNIVTKQGVTPHLH 667
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
QY 389 LASKIG 394
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 668 LASQEG 673

RESULT 3
T15347
ankryrin-related unc-44 - Caenorhabditis elegans
C;Species:Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text change 09-Jul-2004
C;Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
R;Gattung, S.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid B0350.
A;Reference number: Z18332
A;Accession: T15347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2039 <GAT>
A;Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA93444.1
A;Accession: T15346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1000,'SKLOHRT',1002-1718,'KWEELNRL',1727,'D','ES',1942,'PSPAQRS',1950,'IVAES',1956-1957,'EQVPE'
32,'S',2034-2035,'GSTRSVEPERHSHQEDHEGST'<GAA>
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1
A;Accession: T15344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1718,'KW',1903-1905,'NRLADESSPS',1916-1917,'QRSTIVAESETSEQVPE',1934-1935,'EQVPE'
<GAA>
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1
A;Accession: T15345
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1718,'KWEELNRL',1727,'D','ES',1942,'PSPAQRS',1950,'IVAES',1956-1957,'EQVPE'
PTRSVPEPERHSHQEDHEGST'<GAA>
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
R;Otsuka,A.J.; Franco,R.; Yang,B.; Shim,K.H.; Tang,L.Z.; Zhang,Y.Y.; Boontrakulpooon
J. Cell Biol. 129, 1081-1092, 1995

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OM protein - protein search, using sw model

Run on: May 26, 2005, 14:07:29 ; Search time 11.279 Seconds
(without alignments)
3361.064 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
Sequence: 1 MQFFGLVNTFGVTLFSN.....EVDTPNDFGETPTFLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2078	99.7	851	T12503	hypothetical prote
2	332	15.9	3924	S37431	ankyrin 2, neurona
3	318	15.3	2039	T15347	ankyrin-related un
4	313.5	15.0	1549	T13940	ankyrin - fruit fl
5	296	14.2	4377	A55575	ankyrin 3, long sp
6	294	14.1	1856	B35049	ankyrin 1, erythro
7	294	14.1	1880	A35049	ankyrin 1, erythro
8	294	14.1	1881	1 SJRUK	ankyrin 1, erythro
9	293	14.1	1765	T42714	ankyrin 3, splice
10	293	14.1	1940	T42715	ankyrin 3, splice
11	293	14.1	1943	T42713	ankyrin 3, splice
12	293	14.1	1961	T42716	ankyrin 3, splice
13	285	13.7	1848	S37771	ankyrin, erythrocy
14	285	13.7	1862	T49502	ankyrin - mouse
15	281.5	13.5	397	T46445	hypothetical prote
16	258	12.4	1023	T26261	hypothetical prote
17	255.5	12.3	1411	S30355	alpha-latroinsecto
18	249	11.9	791	T42691	hypothetical prote
19	248.5	11.9	1435	T32930	hypothetical prote
20	244	11.7	247	D84448	probable ankyrin l
21	237	11.4	1401	S11527	alpha-latrotoxin p
22	236	11.3	2437	S42612	transmembrane prot
23	234	11.2	1423	1 I37275	death-associated p
24	233	11.2	426	AE2149	hypothetical prote
25	231	11.1	934	1 H71274	probable ankyrin
26	225	10.8	1071	T22327	hypothetical prote
27	218.5	10.5	368	T18184	ankyrin repeat pro
28	216.5	10.4	633	T27499	hypothetical prote
29	216.5	10.4	1184	2 T00253	gene Ankhzn protei

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFP434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12503
R:Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17527
A:Accession: T12503
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <ANS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFP434A102
C:Genetics:
A>Note: DKFP434A102.1

Query Match	99.7%	Score	2078	DB	2	Length	851
Best Local Similarity	99.7%	Pred. No.	1.6e-168				
Matches	393	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
QY	1	MOFFGLVNTFGVTLFSNPRFRKEVAVADYTS	SDRVREEGQLILFQNTPNRTWDCVLV	60			
DB	46	MOFFGLVNTFGVTLFSNPRFRKEVAVADYTS	SDRVREEGQLILFQNTPNRTWDCVLV	105			
QY	61	NPRNSQSGFRLFQLEADALVNFHOYSQQLLP	PFYESSQVLTHTVQLTDLIRNHPSW	120			
DB	106	NPRNSQSGFRLFQLEADALVNFHOYSQQLLP	PFYESSQVLTHTVQLTDLIRNHPSW	165			
QY	121	SVAHLAVELGIRECFHHSRIISCANCAENEG	CTPLHLACRKGDELVELVOYCHTQMD	180			
DB	166	SVAHLAVELGIRECFHHSRIISCANCAENEG	CTPLHLACRKGDELVELVOYCHTQMD	225			
QY	181	VDYKGETVFHVAVQGDNSQVLQLGRNAVAG	LNVNNOGLTPLHLACQLGKQEMVRVLL	240			
DB	226	VDYKGETVFHVAVQGDNSQVLQLGRNAVAG	LNVNNOGLTPLHLACQLGKQEMVRVLL	285			
QY	241	LCNARCNI MGNGYP IHSAMKFSQKCAEMI	ISMDSQIHSKDPRYGASPLHWAKNAEMA	300			
DB	286	LCNARCNI MGNGYP IHSAMKFSQKCAEMI	ISMDSQIHSKDPRYGASPLHWAKNAEMA	345			
QY	301	RMLLKGCNNVTSSAGNTALHVGWNRNFDCA	IVLLTHGANADARGEHTPLHLAMSK	360			
DB	346	RMLLKGCNNVTSSAGNTALHVGWNRNFDCA	IVLLTHGANADARGEHTPLHLAMSK	405			
QY	361	DNVEMIKALIVFGAEVDTTDFGTPTFLASKIG	394				
DB	406	DNVEMIKALIVFGAEVDTTDFGTPTFLASKIG	439				

RESULT 2